Wed Feb

## BEST AVAILABLE COPY

660.5 660 658.5 656.5 656.5 655.5 653.5 us-10-633-835-2.rpr ; Search time 46 Seconds (without alignments) version 5.1.7 - 2006 Biocceleration Ltd. 2006, 18:08:56 using sw model GenCore (c) 1993 4

biotin carboxylase propionyl-CoA carb acetyl-CoA carboxy acetyl-CoA carboxy

F81033 G95929 B64566 AB3352 C83998 B75558 AC2997

acetyl-CoA carboxy probable methylcro

hypothetical prote hypothetical prote

carboxylase biotin carboxylase acetyl-CoA carboxy

biotin

B86722 G87482 D64453

acetyl-CoA carboxy hypothetical prote

ALIGNMENTS

Post-processing:

Database

growth in Ust

A; Gene: ACC1

C.Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin C.Superfamily: human acetyl-CoA carboxylase; biotin binding; ligase
C;Keywords: biotin binding; ligase
E;A1-549 Domain: biotin carboxylase homology <BCH>
E;675-747/Domain: lipoyl/biotin-binding homology <LPB>
F;714/Binding site: biotin (Lys) (covalent) #status predicted A; Introns: 14/1 C; Superfamily: hu C; Keywords: bioti F;41-548/Domain: F;675-747/Domain:

SUMMARIES

Score 2896; DB 1; Length 2185; Pred. No. 1.9e-197; 0; Mismatches 2; Indels 0 99.64; Best Local Similarity Matches 557; Conservative Query Match

120 180 121 181 240 9 61 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKW 61 AYETFGDERAIEFTVWATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERA 62 AYETFGDERALBFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERA GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 1 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKW PWSGTGIKETWMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGI 181 121 à g g ò ò

RRHOKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360 242 RKCTNGEBFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQ 301 RKCTNGEEFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQ PWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGI 182 241 301 셤 ઠે ద ò g 361 RLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESF 420

300

C; Species: Ustilago maydis (corn smut)
C; Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004
C; Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004
C; Accession: \$60200; \$49991
R; Bailey, A.; Keon, J.; Owen, J.; Hargreaves, J.
Mol. Gen. Genet. 249, 191-201, 1995
A; Title: The Acci gene, encoding acetyl-CoA carboxylase, is essential for growth in LA; Reference number: \$60200; MuID:96086936; PMID:7500941
A; Accession: \$60200
A; Molecule type: DMA
A; Residues: 1-2185 <BAI>A; Cross-references: UNIPROT:Q12721; UNIPARC:UPI000006A8BA; EMBL:Z46886; NID:g600097; C; Genetics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 1 PPPDHKAVSQFIGGNPLETA.....LDGLIQDRLTAERPPADLAV Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues summaries Gapop 10.0 , Gapext 0.5 Minimum Match 0% Maximum Match 100% Listing first 45 st Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-10-633-835-2 2907 - protein search, Copyright pirl:\* pir2:\* pir3:\* PIR 80:\* February **BLOSUM62** 

Scoring table:

Searched:

Perfect score:

Sequence:

OM protein

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acetyl-CoA carboxy acetyl-CoA carboxy probable acetyl-Co acetyl-CoA carboxy 1-CoA carboxy 1-CoA carboxy 1-CoA carboxy probable acetyl-Co probable acetyl-Co protein F5J5.19 [i carboxy acetyl-CoA carboxy acetyl-CoA carboxy carboxylase acetyl-CoA carboxy carboxy hypothetical prote otin carboxylase carboxylase acetyl-CoA carboxy Description -COA A35578 S41121 138928 A29924 A29924 T07923 T07920 E86483 T09538 A57710 T07084 T07081 Query Match Length DB 2346 2324 2123 2359 2257 2257 2311 2257 2261 1978 2325 1781 1780 1754.5 1598.5 1581.5 1579 1579.5 1569.5 1558.5 1558.5 1555.5 1543.5 1502.5 769 724 709.5 709.5 679 Score Result No.

Db 362 RLQVEHPTTEM		දි සි	485 GHIFAYGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLI 544 
Qy         421 KTQRKPQPQGH           Db         422 KTQRKPQPQGH	KTORKPOPOGHVVACRITAENPDIGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480	· & 1	ODRITARRPPADIAV 559
Oy 481 DSQFGHIFAYGA 	DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL 540	ഗ	SSS SNALIABERFULLIAV S/S
Oy 541 DGLIQDRLTAERPPADLAV Db 542 DGLICORLTAERPPADLAN	559	T38906 acetyl- C;Speci C:Date:	CoA carboxylase (EC 6.4.1.2) [similarity] - fission yeast (Schizosaccharomyces r es: Schizosaccharomyces pombe 03-Dec-1999 #semmence revision 03-Dec-1999 #text change 09-Jul-2004
8		C; Acces R; Connc submitt	C.Accession: T38906 R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
T30568 acetyl-CoA carboxylase (ECC:Species: Emericella nich		A;Refer A;Acces A:Statu	ence number: Z21813 sion: T3896 s s: preliminary: translated from GB/EMBL/DDBJ
C;Date: 22-Oct-1999 #sequi C;Accession: T30568		A;Molec A;Resid	ule type: DNA ues: 1-2280 <con></con>
R, Morrice, J.; MacKenzie, Curr. Genet. 34, 379-385,		A; Exper	-references: UNIPROT:P78820; UNIPARC:UP10000127CAE; EMBL:Z99261; PIDN:CAB16395.1 imental source: strain 972h-; cosmid c56E4
A;Title: Isolation and ch. A;Reference number: Z2086; A;Accession: T30568	pergil	C;Genet A;Gene: A:Map r	108: SPDB:SPAC56E4.04c osttion: 1
A;Status: preliminary; tr. A;Molecule type: DNA		A; Intro C; Super	ns: 44/1 family: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
A; residues: 1-2200 cmOK) A; Cross-references: UNIPR C:Genetics:	02; PI	ouero Ouero	Tus: Ilgane 71.9%: Score 2090.5: DB 2: Length 2280;
A; Gene: accA A; Introns: 54/3; 111/3	A; Gene: acch A; Introns: 54/3; 111/3	Best Lo Matches	cal Similarity 71.4%; Pred. No. 4.6e-140; 396; Conservative 62; Mismatches 96; Indels
C;Keywords: ligase	YI-COA Carboxytase; blotin carboxytase nomology; lipoyl/blotin-	ò	6 KAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETF 65
Query Match 75.3 Best Local Similarity 74.8	\$; Score 2190; DB 2; Length 2288; \$; Pred. No. 3.88-147; Tall.	ය සි දි	37 RVASHFLGGNSLDKAPAGKVKDYIASHGGHTVITSILIANNGIAAVKEIRSIRKWAYETF 96
Oy 5 HKAVSQFIGGNI	D. T.	중 옵	97 NNERAIKPTVMATPDDLKVNADYIRMADQYVEVPGGSNNNNYANVELIVDIAERMNVHAV 156
Db 19 HNLPSHFIGGN		λΌ	126 WACWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGT 185
65	FGDERAIBFTWATFEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHA 124	ପ୍ର	
79		8	186 GIKETMMSDQ-GPLTVSDDVYQQACIHTAEBGLEKAEKIGYPVMIKASEGGGGKGIRKCT 244
QY 125 VWAGWGHASENI 	VWAGWGHASERPKLPESLAASKHKIIFIGFEGSAMKSLOUKISSTIVAQUADVPCMPWSG 184	å ð	
Qy 185 TGIKETWMSDQ	TGIKETWMSDQGFLTVSDDVYQQACIHTAEBGLEKAEKIGYPVMIKASEGGGGKGIRKCT 244	qq	:  :    :      :
Db 199 TGVDEVKVDENC		ζō	305 KIIEEADVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364
	NGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQ 304	යි දි	337 KIIEEAAVTIAPAATFHEMERAAVRIGELVGYASAGTIEYLYEPENDRFYFLELNPRLQV 396 266 eudpttemmicciniemaal onamatelystettiyomidegneytipensserryn 424
305	36	<b>3</b> 8	EMPTTENVSGVNLPAAQLQVAMGLPLSRIPHIRELXGLPRDGDSEIDFFFQNPESFKVQK
		ζō	425 KPQPQGHVVACRITAENPDIGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQF 484
Qy 365 EHPTTEMVSGVI	EHPITEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQR 424	qa	
Db 379 EHPTTEMVTGVI	NLPAAQLQIAMGIPLHRIRDIRLLYGVDPNTSAEIDPDFSSEESFKTOR 438	λö	485 GHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLI 544
	425 KPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQF 484	අ <sub>ධ</sub> ,	
Db 439 RPQPKGHTTACI	RITSEDPGEGFKPSSGTWHELNFRSSSNVWGYFSVGTAGGIHSFSDSQF 498	ò	545 QDRITABERPPADIAV 559

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    37 RVASHFLGGNSLDKAPAGKVKDYIASHGGHTVITSILIANNGIAAVKEIRSIRKWAYETF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 WAGWGHASENPKLPEMLSASSKKIVFIGPPGSAMRSLGDKISSTIVAOSARVPCMSWSGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456 VPTPKGHCVACRITSEDPGEGFKPSSGMIKDLNFRSSSNVWGYFSVGTAGGIHEFSDSQF
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70.6%; Pred. No. 6.8e-138;
iive 64; Mismatches 97;
                                                                                             DGLIQDRLTAERPPADLAV
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Best Local Similarity 70.6
Matches 392; Conservative
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A. Molecule 'type: DNA
A. Gross-references: UNIPARC:UPI0000145F95; EMBL:M92156; NID:9402313; PIDN:AAA20073.1; PI
C. Genetics:
A. Genes: SGD:ACC1; FAS3; ABF2
A. Genes: SGD:ACC1; FAS3; ABF2
A. Gross-references: SGD:S0005299; MIPS:YNR016c
A. Molecule 'to are a controlled 'to a con
                                                                                                                                                                                                                                    With the fortein Sequence Database, April 1996

A; Reference number: S63346

A; Reference number: S63346

A; Accession: S63347

A; Accession: S63347

A; Residues: 1-223 «POIA*

A; Residues: 1-223 «POIA*

A; Residues: 1-223 «POIA*

A; Cross-references: UNIPROT: Q00955; UNIPARC: UPI0000127CAF; EMBL: Z71631; NID: g1302497; PI
A; Experimental source: strain S288C

B; Al-Peel, W.; Chirala, S.S.; Wakil, S.J.

Broc. Natl. Acad. Sci. U.S.A. 89, 45344538, 1992

A; Title: Cloning of the yeast RAS3 gene and primary structure of yeast acetyl-CoA carbox

A; Reference number: S31249; MUID: 92262474; PMID: 1350093
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                                                                                                      acetyl-CoA carboxylase (EC 6.4.1.2) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N3175; protein YNR016c
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63347; S31249
R;Pohl, T.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 DAVWAGWGHASENPLLPEKLSQSKRKVIFIGPPGNAMRSLGDKISSTIVAQSAKVPCIPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 69.19
Matches 386; Conservative
AQKVTSARPDKMLAV
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A,Accession: S41121
A,Molecule type: mRNA
A,Residues: 1-2339 <HAJ>
A,Residues: 1-2339 <HAJ>
A,Cross-references: UNIPARC:UPI000011EDF5; EMBL:X68968; NID:9452315; PIDN:CAA48770.1; 1
C,Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin C;Keywords: biotin binding; ligase
                                                                                                                                                                                                                                                                                                                        318
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                                                                                                                                                                               278
                                                                                                                                                                                                                                                         279 NVPODLYEKGYVKDVDDGLKAAEEVGYPVMIKASEGGGGKGIRKVNNADDFPNLFRQVQA 338
                                                                                                                                                                                                                                                                                                                                             319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIP 378
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                                                LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                        220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 AENPDIGFKPGMGALTEINFRSSTSTWGYFSVGTSGALHEYADSOFGHIFAYGADRSEAR 498
ASP-AEFVTRPGGNKVIEKVLIANNGIAAVKCMRSIRRWSYEMFRNERAIRFVVMVTPED 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 11-Jan-2002
C;Accession: S41121
                                                                                                                                                            399 VFEHMEQCAVKLAKAVGYVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPCTEMVADVNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 LKANAEYIKMADHYVPVPGGPNNNNYANVELILDIAKRIPVQAVWAGWGHASENPKLPEL
                                                                     TVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLG
                                                                                                                                                                                                                                                                                                                        EVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379 AAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 499 KOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                      LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD----OGFL
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A;Title: Cloning of human acetyl-CoA carboxylase cDNA.
A;Reference number: S41121; MUID:94139704; PMID:7905825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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F:747-819/Domain: lipoyl/biotin-binding homology <LPB>
F:786/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.3%; Score 1782; DB 2;
Best Local Similarity, 63.6%; Pred. No. 4.4e-118;
Matches 344; Conservative 78; Mismatches 105;
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A;Title: Heterogeneity at the 5' end of rat acetyl-coenzyme A carboxylase mRNA: Lipogeni A;Reference number: 155305; MUID:89214151; PMID:2565337
A;Accession: 170069
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Daccession: A35578; A37119; IS9145; I70069; I70070; I55305
R;Lopez-Casilae, F.; Bai, D.H.; Luo, X.; Kong, I.S.; Hermodson, M.A.; Kim, K.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 5784-5788, 1988
A;Title: Structure of the coding sequence and primary amino acid sequence of acetyl-coen A;Reference number: A35578; MUID:88320328; PMID:2901088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 86, 4042-4046, 1989
A;Title: Structural features of the acetyl-CoA carboxylase gene: Mechanism for the gener
A;Reference number: IS9145; MUID:89264558; PMID:2566999
A;Accession: IS9145
                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-2345 <LOP>
A; Residues: 1-2345 <LOP>
A; Cross-references: UNIPROT: P11497; UNIPARC: UP10000127C7B; GB:J03808; NID:g202644; PIDN: A; Cross-references: UNIPROT: P1.8.7; Lopez-Casillas, F.; Kim, K.H.
R; Kong, I.S.; Lopez-Casillas, F.; Kim, K.H.
A; Biol. Chem. 265, 13865-13701, 1990
A; Title: Acetyl-CoA carboxylase mRNA species with or without inhibitory coding sequence A; Reference number: A37119; MUID:90337981; PMID:1974251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UP1000017084D; GB:M26196; NID:g202649; PIDN:AAA40655.1; PID:
A;Accession: I70070
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63.6%; Pred. No. 2.7e-118;
tive +80; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1167-1200 «KON»
A;Cross-references: UNIPARC:UPI000017312F; GB:M55315
A;Experimental source: clone lambdaDHN121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ.
A;Residues: 1-74 <RES>
A;Cross-references: UNIPARC:UPI0000170BB7;
A;Experimental source: hepatic
B;Lopez-Casillas, F; K4m, K.
J Biol. Chem. 264, 7176-7184, 1989
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A;Molecule type: mRNA
A;Residues: 1-33 <RE3>
                                                         Best Local Similarity 63.6
Matches 344; Conservative
                          545 ODRLTAERPPADLAV
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A; Residues: 1-33 <RE2>
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A, Accession: A29337
A, Molecule type: mRNA
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A, Molecule type: MRNA
A, Molecule type: WIPARC: UPI0000171282; GB:X05019; NID:g63021; PIDN:CAA28675.1; PID
A, Accession: A27903
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 493-552,554-783, 'RSPS', 789-820 <TAK3>
A; Cross-references: UNIPARC: UPI000017312B
C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti:
C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology of SF170-620/Domain: biotin carboxylase; liver
F, 120-620/Domain: lipoyl/biotin-binding homology <BCH>
F, 747-819/Domain: lipoyl/biotin-binding homology close
F, 786/Binding site: biotin (Lys) (covalent) #status predicted
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A,Residues: 1-2324 <TAK1>
A,Residues: 1-2324 <TAK1>
A,Cross-references: UNIPROT:P11029; UNIPARC:UP10000127CAB; GB:J03541; NID:g211567; R,Taxai, T.; Wada, K.; Tanabe, T.
FEBS Lett. 212, 98-102, 1987
A,Title: Primary structure of the biotin-binding site of chicken liver acetyl-CoA c A,Reference number: A91375; MUID:87106011; PMID:2879745
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: A29924; A29337; A27903
R;Takai, T.; Yokoyama, C.; Wada, K.; Tanabe, T.
J. Biol. Chem. 263, 2651-2657, 1988
A;Title: Primary structure of chicken liver acetyl-CoA carboxylase deduced i
A;Reference number: A29924; MUID:88139305; PMID:2893793
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63.4%; Pred. No. 6e-118;
cive 81; Mismatches 103; Indels
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2346 cRES>
A;Cross-references: UNIPROT:013085; UNIPARC:UPI0000127C6D; EMBL:U19822; NID:g849082; 1
A;Experimental source: HepG2 cells
C;Genetics:
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R;Abu-Elheiga, L.; Jayakumar, A.; Baldini, A.; Chirala, S.S.; Wakil, S.J.
Proc. Natl. Acad. Sci. U.S.A. 92, 4011-4015, 1995
A;Title: Human acetyl-CoA carboxylase: characterization; molecular cloning, A;Reference number: I38928; MUID:95249602; PMID:7732023
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NiAlternate names: acetyl-Conzyme A carboxylase
C.Species: Homo sapiens (man)
C.Species: 23-Peb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
                                                                                           280 NVPQELYEKGYVKDVDDGLQAAEEVGYPVMIKASEGGGGKGIRKVNNADDFPNLFRQVQA
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LL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSGSGLRVDWQENDFSKRIL
                                                           TVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLG
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F_i615-687/Domain: lipoyl/biotin-binding homology <LPB> F_i654/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                 Best Local Similairy ...-
Matches 326; Conservative
                                                                               Similarity
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S.Supperfamally: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
C;Keywords: biotin binding; ligase
F;1-487/Domain: biotin carboxylase homology <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPARC:UP10000168A89; EMBL:Z48755; MIPS:YMR207c; NID:g736296; PIDN:
Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: UNIPROT: P32874; UNIPARC: UP1000017627C; EMBL: 249809; MIPS: YMR207C; Experimental source: strain AB972; Note: the published sequence extends beyond the amino end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Residues: 1-510,'L',512-799 <KEA>
Cross-references: UNIPARC:UPI000017627D; EMBL:Z22558; NID:g296212; PIDN:CAA80280.1;
Note: the published sequence extends beyond the amino end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable acetyl-CoA carboxylase (EC 6.4.1.2) HFA1 - yeast (Saccharomyces cerevisiae) NyAlternate names: protein YM8261.01c; protein YM8325.08c; protein YMR207c C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 08-Jul-1995 #sequence revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: S55089; S41802; S59447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t
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submitted to the EMBL Data Library, April 1993
Apescription: Identification of an Saccharomyces cerevisiae gene closely related
A;Reference number: $41802
A;Accession: $41802
      LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETWMSD---QGFL 198
                         222 L--HKNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWNGSGLRVDWQENDLQKRIL 279
                                                                                                                                                               EVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPED 318
                                                                                                                                                                                      340 EVPGSPIFVMRLAKOSRHLEVQILADQYGNAISLFGRDCSVQRRHQKIIEEAPASIATSV 399
                                                                                                                                                                                                                                            378
                                                                                                                                                                                                                                                               400 VFEHMEQCAVKLAKANGYVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPCTEMVADVNLP 458
                                                                                                                                                                                                                                                                                                                          AAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDPDFSSPESFKTQRKPQPQGHVVACRIT 438
                                                                                                                                                                                                                                                                                                                                                                 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ispecies: Saccharomyces cerevision of Dec-1997 #text_change 09-Jul-2004; Accession: 855089; 841802; 85947 #text_change 09-Jul-2004; Accession: 855089; 841802; 85947 #text_change 09-Jul-2004; Accession: 855089; Bowman, S. dubnitted to the EMBL Data Library, June 1995; Reference number: 855089
                                                                                                        280 NVPQELYEKGYVKDADDGLRAAEEVGYPVMIKASEGGGGKGIRKVNNADDFPNLFRQVQA
                                                                                                                                                                                                                                                                                                                                               ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP
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submitted to the EMBL Data Library, March 1995
A;Reference number: S59441
A;Recession: S59447
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Residues: 1-833 <DED>
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Residues: 812-2123
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A, Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA A, Pathway: fatty acid biosynthesis
A, Pathway: fatty acid biosynthesis
C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin C, Keywords: cytosol; ligase
F, 36-542/Domain: biotin carboxylase homology < BCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 IFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESG 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Brassica napus (rape)
.Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 LFGRDCSIQRRHQKIIBEAPVTITKPETFQRMERAAIRLGELVGYVSAGTVEYLYSPKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 EFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFE
                                                                                                                                                                                                                                                                                                                                                               HADVPCMPWSGTGIKETMMSDQ--GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKA
                                                                                                                         54 IRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLI
                                                                                                                                                           Gaps
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R;Schulte, W.; Toepfer, R.; Stracke, R.; Schell, J.; Martini, N.
R;Schulte, W.; Toepfer, R.; Stracke, R.; Schell, J.; Martini, N.
Proc. Natl. Acad. Sci. U.S.A. 94, 3465-3470, 1997
A;Title: Multi-functional acety1-coenzyme A carboxylase from Brassica A;Reference number: Z16220; MUID:97250561; PMID:9096417
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55.0%; Score 1598.5; DB 2;
Best Local Similarity 53.9%; Pred. No. 7.6e-106;
Matches 306; Conservative 92; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetyl-CoA carboxylase (EC 6.4.1.2) A - rape (fragment)
60.4%; Score 1754.5; DB 2; 65.2%; Pred. No. 3.4e-116; ive 78; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || |:||||| || |:::
SNNISTGWLDDLILKNLSSD 491
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Cjaccesion: E86483
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons Chin, C.W.; Chung, M.K.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
M; Huizar, L.
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wenter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFTVMATPEDLKVNADYIRWADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGH 131
                                                                                                                                                                                            286 PPGSSLVTIPBEMYRQACVYTTEEAVASCQVVGYPAMIKASWGGGGKGIRKVHDDDEVRA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                           ASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETM 191
                                                                                                                                                                                                                                                                                                                                                                                                                    312 VTIAPEDARESMEKAAVRLAKUVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEM 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable acetyl-CoA carboxylase, 9984-22276 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                          MSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQ
                                526 CVAVRVISEDPDDGFKPISGQVQELSFKSNPNVWGYFSVKSGGGIHEFSDSQFGHVFAFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 VSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGH
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646 RPPWYLSV 653
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A,Molecule type: DNA
A,Residues: 1-2359 <STO>
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A;Pathway: fatty acid biosynthesis
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
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                                                                            AYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERA 120
                                                                                                  GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180
                                                                                                                                                                                 RRHQKIIBEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDF6SPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVG 471
                           probable acetyl-CoA carboxylase (EC 6.4.1.2) - rape C;Species: Brassita napus (rape) C;Species: Brassita napus (rape) C;Species: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004 C;Accession: T07920 R;Schulte, W.; Schell, J.; Toepfer, R. Plant Physiol. 106, 793-794, 1994 Plant Physiol. 106, 793-794, 1994 Plant Physiol. 106, 793-794, 1994 Plant Physiol. 206217; MUID:95083764; PMID:7991694
                                                                                                                                                                                                                                           PWSGTGIKETWMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVM1KASEGGGGKGI
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PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAA
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-2304 <SCH>
A; Cross-references: UNIPROT: Q42617; UNIPARC: UPI00000A5000;
A; Experimental source: cv. Aklea
C; Genetics:
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Cydecesion: T09538
R;Shorrosh, B.S.; Dixon, R.A.; Ohlrogge, J.B.
Proc. Nacl. Acad. Sci. UV.S.A. 91, 4323-4327, 1994
A;Title: Molecular cloning, characterization, and elicitation of acetyl-CoA carboxylass, A;Title: Molecular cloning, characterization, and elicitation of acetyl-CoA carboxylass, A;Reference number: A58381; MUID:94240129; PMID:7910406
A;Residues: 1-2257 <SHO>
A;Residues: 1-2257 <SHO
A;Residues
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C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                        123 AVWPGWGHASENPELPDALDAK--GIIFLGPPASSWAALGDKIGSSLIAQAADVPTLPWS
                                                                                                                                                                                                                                                                                      TFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVH
                                                                                                                                                                                GTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKC
                                                                                                                                                                                                                                                              244 INGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRH
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A;Map position: 1
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
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                                                            VNGYHSDVVPGRNVAEVNEFCKALGGKRPIHSILVATNGMAAVKFIRSVRTWAYETFGSE
                                      RAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAG
                                                                                                                    WGHASENPRLPESLAASKHK-IIPIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGI
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A57710
acetyl-CoA carboxylage (EC 6.4.1.2) - wheat
coperate acetyl-CoA carboxylage (EC 6.4.1.2) - wheat
coperate: Triticum aestivum (common wheat)
Coperate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Coperation: A57710
Coperation: A57710
Coperation: A57710
Coperate: U.S.A. 91, 6860-6864, 1994
Accession: A57710
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Accession: A57710
Coperation: Description acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
Coccession: Accession:                                                     C;Function:
A;Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
A;Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
A;Pathway: fatty acid biosynthesis
A;Pathway: fatty acid biosynthesis
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology carboxylase
B;134-640/Domain: biotin carboxylase homology cAPB>
F;767-839/Domain: lipoyl/biotin-binding homology cLPB>
F;806/Binding site: biotin (Lys) (covalent) #status predicted
A;Introna: 69/1; 90/2; 209/3; 278/3; 332/3; 363/3; 395/3; 453/3; 485/1; 547/3;
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 ESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIK---ETWMSDQG 196
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467 LPAAQVAVGMGIPLWQVPEIRRFYGMDNGGG----YDIWRKTAALATPFNFDEVDSQWPK 522
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Matches 297,
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Residues: 'WRTYM',1771-2026,'K',2028-2073,'F',2075-2108,'V',2110-2120,'L',2122,'A',212
Cross-references: UNIPARC:UP100000ABB05; EMBL:223038; NID:9396278; PIDN:CAA80573.1; PI
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A;Residues: 1847-1852.'E',1854-1863;1847-1962,'D',1964;2085-2091,'HL';2139-2155,'I',2157
A;Cross-references: UNIPARC:UP100001552CB; UNIPARC:UP100001552CD; UNIPARC:UP1000017627P;
C;Genetics:
A;Gene: Acc-1
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A;Residues: 1-2311 «GORL»
A;Cross-references: UNIPROT:048959; UNIPARC:UPI00000A9808; EMBL:AF029895; NID:g2827149;
A;Experimental source: cv. Hard Red Winter Tam 107, light-grown seedlings
A;Accession: T06162
A;Status: preliminary; translated from GB/EMBL/DDBJ
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N;Alternate names: acetyl-coenzyme A carboxylase
C;Species: Triticium aestivum (common wheat)
C;Date: 05-Nov-1999 #sequence revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T061E1; T061E2; S42660; S78600; S55959
R;Gornicki, P.; Faris, J.; Podkowinski, J.; Gill, B.; Haselkorn, R.
Proc. Natl. Acad. SGi. U.S.A. 94, 14179-14184, 1997
A;Title: Plastid localized acetyl-CoA carboxylase of bread wheat is encoded by
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A; Cross-references: UNIPARC:UPI00000A5F07; EMBL:AF029897; NID:g2827153; PIDN:A
A; Experimental source: cv. Hard Red Winter Tam 107, 1ight-grown seedling
A; Exborough, K.M.; Simon, J.W.; Swinhoe, R.; Ashton, A.R.; Slabas, A.R.
Plant Mol. Biol. 24, 21-34, 199
A; Title: Studies on Wheat acetyl CoA carboxylase and the cloning of a partial
A; Reference number: S42660; MUID:94154234; PMID:7906561
A; Molecule type: mRNA
                                                                                                                                                                        ESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLT
                                                                                                                                                                                                                                                                             VSDDVYQQAÇIHTABEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGE
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C; Function:
A; Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
A; Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
A; Description: catalyzes the ATP-dependent carboxylase homology; lipoyl/biotin
C; Superally: human acetyl-CoA carboxylase; biotin carboxylase homology cataly
C; Keywords: ligase
F; 41-547/Domain: biotin carboxylase homology cataly
F; 713/Binding site: biotin (Lys) (covalent) #status predicted
                               A;Gene: ACCase-A
A;Introns: 116/3; 185/3; 239/3; 270/3; 302/3; 360/3; 391/3; 454/3; 471/3; 485/3; 526/3
5/3; 1466/3; 1525/3; 2243/3
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A;Cross-references: UNIPROT:Q39849; UNIPARC:UPI00000A024A; EMBL:L48995; NID:g1066856;
A;Experimental source: strain Williams 82; leaf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VACRITAENPOTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFD-----FSSPESFKTQRKPQPQGHV 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGE
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
53.6%; Score 1558.5; DB 2; Length
Best Local Similarity 53.6%; Pred. No. 3.4e-102;
Matches 293; Conservative 98; Mismatches 141: The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the sta
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Tabour 100

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C) Species: Glyche max (soybean)

C) Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C) Accession: T07084, T07083

A) Title: Genomic sequence for a nuclear gene encoding acetyl-coenzyme a carboxylase in E

A) Reference number: 215907

A) Reference number: 215907

A) Accession: T07084

A) Status: translated from GB/EMBL/DDBJ

A) Accession: T07084

A) Status: translated from GB/EMBL/DDBJ

A) Residues: 1-2261 <LIU>
A) Accession: T07084

A) Residues: 1-2261 <LIU>
A) Accession: T07084

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A) Residues: 1-21500000008368; EMBL.149020; NID:g1066888; PIDN:AAR81579.1; E

A) Residues: 241-386, N', 988-1356, P', 1358-1458, T', 1460-1650, P', 1652-1781, V', 1783-1857

A) Experimental source: cultivar Lambe rt, leaf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTA '550
                                                                                                                                                                                                                                                                                                                                         KVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESL 142
                                                                                                                                                                                                                                                                                                                                                                  AASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIK---ETMMSDQGFLT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGE 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 VPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDA 319
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                                                                                                                                                                                                               23 SPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDL 82
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                         56;
                                                                                         Length 2257;
                                                                                         53.8%; Score 1565; DB 1; Length 2
54.6%; Pred. No. 1.2e-102;
ive 91; Mismatches 132; Indels
F;661-733/Domain: lipoyl/biotin-binding homology <LPB>
F;700/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                   Query Match
Best Local Similarity 54.61
Matches 300; Conservative
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A;Introns: 25/1; 729/1
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti:
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Best Local S
Matches 294
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C,Genetics:
A,Gene: ACCase-B
A;Gene: ACCase-B
A;Introns: 116/3; 185/3; 239/3; 270/3; 302/3; 360/3; 391/3; 454/3; 471/3; 484/3; 526/3; 5/3; 1464/3; 1524/3
C;Function:
A;Description: catalyzes ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA A;Pathway: fatty acid biosynthesis
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C;Keywords: ligaes
C;Keywords: ligaes
C;K
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A;Residues: 1-2325 <EGL>
A;Cross-references: UNIPROT:Q41743; UNIPARC:UPI00000A4B72; EMBL:U19183; NID:g1045304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139
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Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDLKVNADYIRMADQYVEVPGGSINNINYANVDLIVDVAERAGVHAVWAGWGHASENPRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSDDVYQQACIHTABEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGE
                                                                                                                                                                                                                                                                                                                                                                                                        20 APASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATP
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                                                                                                                                                                                                                                                                                                       Length 1978;
                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.2%; Pred. No. 4.6e-102;
Matches 291; Conservative 100; Mismatches 141; Indels
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R;Egli, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G. Plant Physiol. 108, 1299-1300, 1995
A;Title: A maize acctyl-coenzyme A carboxylase cDNA sequa A;Reference number: Z14632; MUID:95357420; PMID:7630949
A;Accession: T02235
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N;Alternate names: acetyl-coenzyme A carboxylase
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Cispecies: Cyclotella cryptica
Cispecies: Cyclotella cryptica
Cipate: 10-Sep-1999 #text_change 09-Jul-2004
Cipate: 10-Sep-1999 #text_change 09-Jul-2004
Cipate: 10-Sep-1999 #text_change 09-Jul-2004
Cipate: 10-Sep-1999 #text_change 09-Jul-2004
Ricession: A48757
Ricession: Chem. 268, 19534-19559, 1993
A;Title: Cloning and characterization of the gene that encodes acetyl-coenzyme A carbo: A;Reference number: A48757, MUD:93374903; PMID:8103514
A;Accession: A48757
A;Status: precliminary; nucleic acid sequence not shown
A;Residues: 1-2089 <ROBs
A;Residues: 1-2089 <ROBs
A;Residues: 1-2089 cROBs
A;Cross-references: UNIPROT:039478; UNIPARC:UPI00000A5A26; GB:L20784; NID:g1065903; PI)
A;Note: authors translated the codon GCC for residue 1834 as Ala
A, Experimental source: strain A188; leaf
C, Function:
A, Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
A, Pathway: fatty acid biosynthesis
C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti
C, Swpworfamily: human acetyl-CoA carboxylase, biotin carboxylase homology; lipoyl/bioti
P;134-640/Domain: biotin carboxylase homology <B;767-839/Domain: lipoyl/biotin-binding homology <LPB>
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                                                                                                                                                                                                                                                                          Length 2325;
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al Similarity 53.5%; Pred. No. 4.2e-101;
294; Conservative 94; Mismatches 141;
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A; Molecule type: DNA
A; Residues: 1-1657 <WIL>
A; Cross-references: UNIPROT: Q9XUC3; UNIPARC: UPI000007BB00; EMBL: Z82285; PIDN: CAB05298.
A; Experimental source: clone T28F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 4
A;Introns: 32/3; 79/1; 153/1; 248/3; 314/3; 415/2; 520/3; 580/3; 665/3; 698/2; 988/3;
                                       17
                                                                                                                                                                                                                                                                                                                                                286
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                PDIRTI--VVSGNSLTNDAADQYESMEQFIHSHVADIEKRR----PIKRLLVATNGIAAM
                                                                                                                                                            P-----IDGDSELPDEVLVDTKL----HAIAARITCENPDDSFRPSTGKVYEINFPSSQ
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                                                                       ----SPVADFIRKQGGHSVITKVLICNNGIAAV
                                                                                                                                         KEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMAD-QYVEVPGGSNNNNYANV
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       Length
                                       161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T28F3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
   ; Score 1314; DB 2;
; Pred. No. 7.6e-85;
84; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                     3 PDHKAVSQFIGGNPLETAPA--
     45.2%;
ilarity 49.4%;
Conservative E
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submitted to the EMBL Data
A,Reference number: Z20032
A,Accession: T25421
     Query Match
Best Local Similarity
Matches 276; Conserv
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Koseules: 1-2054 <GGE>
A;Cross-references: UNIPROT: Q9GZI3; UNIPARC: UPI0000075897; EMBL: AF025469; PIDN: AAB71048.
A;Experimental source: strain Bristol N2; clone W09B6
A;Genetics:
A;Gene: CESP: W09B6.1
A;Map position: 2
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A,Introns: 18/3; 50/3; 97/1; 734/2; 793/3; 1975/2; 2037/2
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
C;Reywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G--TIPMEIFNKGLVTSADEAVIVANKIGWENGIMIKASEGGGGKGKIRFVDNEADLRNAF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 VQVSNEVIGSPIFLMQLCKNARHIEVQIVGDQHGNAVALNGRDCSTQRRPQKIFEEGPPS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                                                                                                                                                                                                                           LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGT-----GIKETMMSDQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVNIPAAQLQVAMGIPLYSIRDIRTLYGM-DPRGNEVIDFDFSSPESFKTQRKPQPQGHV 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 NAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVT 313
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                                                                                                                                                     ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                                                                                                                                                                                                                                             GFLTVSDDVYQQACIHTAEEGLEKAEKIGYP--VMIKASEGGGGKGIRKCTNGEEFKQLY
                                                                                                                       Gaps
                                                                                       Length 2089;
                                                                                                                       21;
C;Keywords: blotin binding; ligase homology <BCH> P:99-603/Domain: blotin carboxylase homology <BCH> F:711-803/Domain: lipoyl/biotin-binding homology <LPB> F;7170/Binding site: blotin (Lys) (covalent) #status predicted
                                                                                                                       Indels
                                                                                       DB 1;
                                                                                   51.7%; Score 1502.5; DB 1;
llarity 53.2%; Pred. No. 3e-98;
Conservative 95; Mismatches 140;
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MPSHLVV 615
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                                                                                  Query Match
Best Local Simil
Matches 291; C
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Diotin carboxylase - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Accession: A69123
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Cint, D.R.; Doucette-Stamm, L.A.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fur
                                                                                                                                                                                                                                                                                                                                                                                                                                                UNIPARC:UPI0000132BC1; GB:AE000942; GB:AE000666; H
                    107
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 192 MSDQGFLTVSDDVYQQACIHTAEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAK 332
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                                                                                                                                                                                                                                                                                                                                                                                                     not shown
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                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A69123
A; Status: preliminary; nucleic acid sequence not shown; translation : A; Molecule type: DNA
A; Residues: 1-491 < MTH>
A; Residues: 1-491 < MTH>
A; Residues: UNIPROT: 027939; UNIPARC: UPI0000132BC1; GB: AB000994; Experimental source: strain Delta H
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: biotin carboxylase, biotin carboxylase homology;4-450/Domain: biotin carboxylase homology <BCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 KRALSEYIILG-VKTTIPFHKAIMRNEAFRRGELHTHFVD 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 VISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 724; DB 2;
Pred. No. 9.5e-44;
                                                                                         346 LFKOVOGEVPGSPIFIMKVASOSRHL 371
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Best Local Similarity 34.4%;
Matches 179; Conservative 8:
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354 IT-
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C;Superfamily: P;4-450/Domain:
                                                                       252
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;Residues: 1-371 <SCH>
;Cross-references: UNIPROT:004850; UNIPARC:UPI000009F1F2; EMBL:Y10302; PIDN:CAA71347.1
;Experimental source: cv. Akela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pathway: fatty acid blosynthesis
Note: probably chloroplast isoform
Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
Keywords: chloroplast; ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
                                                                       436
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                                                                                                                                                                                                                 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP 378
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probable acetyl-CDA carboxylase (EC 6.4.1.2), chloroplast - rape (fragment) C;Species: Brassica napus (rape)
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T07938
R;Schulte, W.
submitted to the EMBL Data Library, December 1996
                                                LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIK-ETMMSDQGFLTV
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; Pred. No. 3.9e-47;
57; Mismatches 67; Indels
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Best Local Similarity 51.9%;
Matches 138; Conservative 5
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Accession: T07938
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272

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us-10-633-835-2.rpr

strain

10;

93;

Length 447; Indels 159

--EGLVETEQEGLEL 148

208

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A;Cross-references: UNIPROT:Q06862; UNIPARC:UPI00001251AA; GB:L14862; NID:g289132; PIDI C$Superfamily: blotin carboxylase; blotin carboxylase homology C;Keywords: ATP; ligase F;5-447/Domain: blotin carboxylase homology <BCH>
Title: Genes for two subunits of acetyl coenzyme A carboxylase of Anabaena sp. Reference number: A53311; MUID:93352435; PMID:8102363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 RSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEKIGYPVMIKASEGGGGKGIRKCTNGEBFKQLYNAVLGEV----PGSPVFVMKLAGQAR 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 EPASAKSYLNIPNIIAAALTRNASAIHPGYGFLSENAKFAEICA--DHHIAFIGPTPEAI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 YVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRD 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 YTGAĞTIBFLLD-RSĞQFYFMEMNTRIQVEHPVTEMVTĞVDLLVEQIRIAQĞERLRLTQD 327
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                                                                                                                                                                                                                                                                                        'Match 24.4%; Score 709.5; DB 2; Local Similarity 32.9%; Pred. No. 9e-43; es 170; Conservative 88; Mismatches 165;
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                                                                                                      A; Molecule type: DNA
A; Residues: 1-447 <GOR>
                                                                             A; Status: preliminary
                                                       A;Accession: A53311
                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 170;
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           RESULT 26
AH1923
bjotin carboxylase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Apecies: Nostoc sp. strain PCC 7120
A;Note: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH1923
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Rese. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Reference number: AH1923
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 <KUR>
A;Residues: 1-447 <KUR>
A;Residues: 1-447 <KUR>
A;Experimental source: strain PCC 7120
C;Genetics:
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C;Superfamily: biotin carboxylase; biotin carboxylase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.4%; Score 709.5; DB 2; 32.9%; Pred. No. 9e-43; iive 88; Mismatches 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 32.9
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 QVVL
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probable acetyl-CoA carboxylase (EC 6.4.1.2) biotin carboxylase chain NWA0596 [similar: N; Contains: biotin carboxylase (EC 6.3.4.14)
C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Accession: H81978
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morr; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrean Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MUID: 20222556; PMID: 10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9JW07; UNIPARC:UPI00000C49E5; GB:AL162753; GB:AL157959; A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: accC; NMA0596
C;Superfamily: biotin carboxylase; biotin carboxylase homology
LRECAITG-LPTTIGFHQRIMENPQFLQGNVSTSFV 442
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A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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Abjorin carboxylase (EC 6.3.4.14) - Anabaena sp. (strain PCC 7120)

NiAlternate names: acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxylase chain cispecies: Anabaena sp.
C; Species: Anabaena sp.
C; Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: A53311
R;Gornicki, P.; Scappino, L.A.; Haselkorn, R.
J; Bacteriol: 175, 5268-5272, 1993
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homology

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C;Superfamily: biotin carboxylase; biotin carboxylase F;4-450/Domain: biotin carboxylase homology <BCH>
                                                                                 23.3%;
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A; Residues: 1-506 < KLE>
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                                                                                                    Local Simi
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Ds.Dec.1997 #sequence_revision 05-Dec.1997 #text_change 09-Jul-2004
C;Accession: A65581
R;Kunst, F: Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G:; Azevedo, V.; Berter
C; Bron, S:; Broullet, S:; Bruschi, C.V.; Caldwell, B:; Capuano, V:; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.
Nature 390, 249-256, 1997
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sera
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Voshida, K.; Watunore: P.; Wippat, A.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Aluthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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                                                                                                                                                                                                                                                             EVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPG 156
                                                                                                                                                                                                                                                                                                                                                               SAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---QVEGHAFECRINAEDP-YNFIPSPG 352
                                                                                                                                                                                                                                                                                                             CIGPAASAQSYLNVPAIIAAAEVSCADAVHPGYGFLAENADFAEQVEQS--GFTFIGPKP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQ---LYNAVLGEVPGSP-VFVMKLAG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPRHVEIQVIADEHGNAVYLAERDCSLORRHOKVIEEAPAPFITEKERAKIGKACADACK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 ALTELNFRSSTSTWGYFSVGTSGALHE-----YADSQFGHIFAYGADRSEARKQMVISL 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIESCHLPSG-----FGIRVDSHIYQGYRIPPYYDSLIGKVCVVGKDRDQAMAKWRVAL 406
                                                                                                                                                                                                           49
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                                                                                                                                                                                           333 LVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIPAAQLOVAMGIPL-Y
                                                                                                                                                         37 VITKVLICHNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QARHLEVQLLADQYGNA1S1FGRDCSVQRRHQK11EEAPVT1AFEDARESMEKAAVRLAK
                                                            Length 453;
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                                                                                                                                                                                                                                                                                                                                                                                              90; Mismatches 176;
                                                          23.4%; Score 679; DB 2; 32.6%; Pred. No. 1.4e-40;
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1 MLKKVLIANRGEIALRVLRACREMGIAT-
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C, Genetics:
A, Gene: accC
                                                                                                         Conservative
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KQKDI-----
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170; Conserv
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C, Keywords: ligase
                                                       Query Match
Best Local S
Matches 170
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Diotin carboxylase (acc) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69277
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dods:
C;Accession: D69277
R;Klenk, H.P.; Clayton, R.J.; Ouackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa.
A;Reference number: A69250; MUID:98049343; PMID:9389475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 YSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGM 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QGIIENVEEA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 GEIKMYLPPGGLGVRVDSAAYPGY-----SIPPYYDSMIAKVITYGKTRDEALARMKR 406
                                                                                                                                                                                                                                                                                                                                                         50 CIGPKASKDSYLNVTNIVSVAKLTGTDAIHPGYGFLAENADFAE--LCEEVNVTFVGPSP 107
                                                                                                                                                                                                                  49
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A,Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                    EVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPG
                                                                                                                                          37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYV
                                                                                                                                                                                                           --VAVYSEADKDALHVOMADEAF
                                                                                                                                                                                                                                                                                                                                                                                                                              SAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEKAEKIGYPVMIKASEGGGGKGIR-----KCTNGEEFKQLYNAVLGEVPGSPVFVMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EGWAIECRINAENPSKNFMPSP
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                                                                            88;
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       Length
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; Score 676; DB 2; L; Pred. No. 2.2e-40; B1; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 SLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLD
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llarity 33.7%; Pred. No. 3.1e-40;
Conservative 83; Mismatches 165
                                                                                                                                                                                                               1 MIKKLLIANRGEIAVRIIRACRELGIET--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 DAISKMGTKDVARETMKQAGVPIVPGS
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Diotin carboxylase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: J2-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: G71860
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R. Javes, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jing, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pala A;Reference number. A71800; MUID:99120557; PMID:9923682
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-455 <ARN>
A;Experimental source: strain J99
C;Genetics:
C;Genetics:
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--- PGLIESEATALKI 148
                                                                                                                                                                                                                                                                                                                              336 YVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTŢEMVSGVNIPAAQLQVAMGIPLYSIRD 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AYLPPGGPGVRIDSHVYTDYEIPPYYDSLIGKLIVWAGDRPSAIKRMORA 407
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                                                                                                    456 LNFRSSTSTWGYFSVGTSGA-----LHEYADSQFGHIFAYGADRSEARKQMVIS
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13 LSRILIANRGEIALRAIQTIQEMGKES------IAIYSIADKDAHYLNTANAKVC
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                                                                                                                                                                                                                                                                                                                                                                 269 YVGAGTVEFLVD-GNGNPYFMEMNTRIQVEHPVTEMITGYDLISEQIRIAMG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 IRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMGALTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 ITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADOYVE
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                                                                 AEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVP---GSP-VFVMKLAGQAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: biotin carboxylase; biotin carboxylase homology F;15-455/Domain: biotin carboxylase homology <BCH>
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112 TAMGDKSTAKKTMQKSGVPCVPGS-
                                                                                                                                                                                              276
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574380

biotin carboxylase accC - Synechocystis sp. (strain PCC 6803)

N/Alternate names: hypothetical protein sll0053

C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                     - IDTVDEAKEWAEKIGYPVAVKASGGGGGIGIVVVNSQEELEEAFRKSKKLGESYFKDST 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324
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                           IRMADOYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQV 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDT 444
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                                                                                                                                                                                                                                                                                            CIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCINGEEFKQLY--NAVLGE--VPGSP
                                                                                                                                                                                                                                                                                                                                                                                                                            VFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESME
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A;Accession: S74380
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DMA
A;Molecule type: DMA
A;Residues: 1-448 <KAN>
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C;Superfamily: biotin carboxylase; biotin carboxylase homology
F;5-448/Domain: biotin carboxylase homology <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94; Mismatches 167; Indels
                                                                                                                                                                                                                      IVFIGESPEVIRIAGSKVRSRESMQRAGVPVIPGSPK-----
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8 8	RDIRTLYGMDPRGNEVIDFDFSSPESFKTORKPOPQGHVVACRITAENPDTGFKPGMGAL 45	Qy 506 KELSIRGDFRITVEYLIKLETDAFESNKITTGWLDGLIQDR 547      :
qa	CRITAEDPKK-FYPSPGKI 365	
oy Op	454 TELNFRSSTSTWGYPSVGTSGALHEYADSOFGHIFAYGADRSEARKGMVISLKE 507	RESULT 34 G95929 probable methylcrotonoyl-CoA carboxylase (EC 6.4.1.4),[imported] - Sinorhizobium melil
ò	SOB LSIRGDFRITVEYLIKLLETDAFESNKITTGWLD S41	C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 31-Dec-2004 C:Acression: G56929
q	iemlenadfroakihtryle 452	R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hern Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 A:Title: The complete sequence of the 1.683-kb pSvmB megaplasmid from the N2-fixing en
RESULT F81033		A;Reference number: A95842; MUID:21396508; PMID:11481431 A;Accession: G95929
acetyl- C,Speci C,Date:	ningitidis (	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-662 <kur></kur>
C, Acces R, Tette	; Eisen, J.A	A;Cross-references: UNIPROT:Q92VJ8; UNIPARC:UP100000CB61A; GB:AL591985; PIDN:CAC49103. A;Experimental source: strain 1021, megaplasmid pSymB
ri, H.	herty, B.A.; a, M.	R;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Huble pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F T. Hyman P. W. Jones T.
A; Autho A; Title	ouoli, R.; Ve in MC58.	Science 293, 68-672, 2001 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaur
A;Refer A;Acces A;Statu	A;Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: F81033 A;Status: preliminary	hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A,Fille: The composite genome of the legume symbiont Sinorhizobium meliloti. A.; Reference number: A96039; MUID:21366234; PMID:11474104
A, Molec A, Resid		A; Contents: annotation C; Genetics:
A; Cross A; Exper	E002098; NID	A;Gene: mccB; SMb21124 A;Genome: plasmid C.Sunerflamilu. himan acetyl-fold carboxylase, hiotin carboxylase homology; linovl/bioti
A; Gene: C; Super		C;Keywords: ligase
Query Best	Query Match 22.9%; Score 667; DB 2; Length 453; Best Local Similarity 32.4%; Pred. No. 9.7e-40;	Query Match 22.9%; Score 666; DB 2; Length 662; Best Local Similarity 33.1%; Pred. No. 2e-39; Matches 176; Conservative 84; Mismatches 195; Indels 76; Gaps 12;
Match	, Conservat	37 VITKVLICNNGIAAVKEI
රි සි	37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYV 96 1:	: : :       : :       :   :  :     : :       : :     : :     : :
3 8		OY 97 EVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPG 156
: a	SO CIGPAASAQSYLNVPAIIAAAEVSCADAVHPGYGFLAENADFAEQVEQSGFTFIGPKP 107	50 RIGGAPAAESYLASAPIVQAARSVGAQAIHPGYGFLSENADFAEAVAEAGMIFVGPPP
ò	GTGIKETMMSDQGFLTVSDDVYQQACIHTAEEG 21	OY 157 SAMESLORKISZTIVAOQHADVPCMPMSGTOIKETMMSDQGFLTVSDDVYQQACIHTAEEG 216 1
සි දි	108 DTIRLMGDKVSAKHAMIAAGVPCVPGSDGALPDDGEEI 145 217 LEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKOLYNAVLGEVPGSP-VFVMKLAG 272	Qy 217 LEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVFVWKLAG 272
; a		146 - DRAREIGYPVLIKARAGGGGKGMRRVERQEDFGPALEAARREAESAFGDGSVLLERYLT
ò	OARHLEVOLLADOYGNAISIFGRDCSVORRHOKIIEEAPVTIAPEDARESMEKAAVRLAK	Oy 273 QARHLEVQULADOYGNAISIFGRDCSVQRRHQKIIBEAPVTIAPEDARESMEKAAVRLAK 332
qq	206 RPRHVEIGVIADEHGNAIYLAERDCSLORRHOKVIEBAPAPFITEKERAKIGNACADACK 265	333
රු සි	333 LVGYVSAGTVEWLYSPESGEPAFLELNPRLQVEHFTTEMVSGVNIPAAQLQVAMGIPL-Y 391	265
Š	SIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMG	389 PLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPGGHVVACRITAENPDIGFKP
g	324 KQKDI	Db 325 PL

PIDN: AAL51981.

12

Gaps

91;

Length 667; Indels 96

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C;Accession: AB3352.
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova a.; Mazur, M.; Goltsman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lete: Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melite; A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                      мар ровітіон: і
Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGS----PVFVMKLAG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 RLTRYRPPVEGRNPDGTVIRNDT---GVFE---GGEISMYYDPMIAKLCTWGPDRISAID 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 EVPGGSNNNNYANVDLIVDVAERAGVHAVWACWGHASENPRLPESLAASKHKIIFIGPPG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 OPRHIBIOVLGDOHGNVYYLGERECSIORRNOKVIEEAPSPFLDEATRKAMGEQAVALAK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 AVGYYSAGTVEFIVD-GNRNPYFLEMNTRLQVEHPVTELITGIDLVEEMIRVASGEKLRF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 ALTELN------FRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARK 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 LVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPL-Y 391
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 SIRDIRTLYGMDPRGNEVIDFDSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMG
                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:Q8YHJ8; UNIPARC:UPI0000057E0A; GB:AE008917; A,Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 NAIDAMGDKITSKKLAAEAGVSTVP-------GHMGLIED-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.7%; Score 660.5; DB 2; 32.2%; Pred. No. 5e-39; iive 85; Mismatches 177;
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Matches 168; Conservative
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                                                                                                                                                                                                                                                                    A; Residues: 1-667 < KUR>
                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
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C;Superfamily: huma
C;Keywords: ligase
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Cipate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

Cipate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

Cipate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

Cipate: 09-Aug-1997 #sequence_revision 0-Aug-1997 #text_change 09-Jul-2004

R.Tomb, J.F. White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujli, C.; Bowman, C.; Watthey, L.

Nature: 388, 539-547, 1997

A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A.Atitle: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A.Accession: B64566

A.Accession: B64566

A.Accession: preliminary; nucleic acid sequence not shown; translation not shown

A.Residues: 1-458 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:025134; UNIPARC:UP100000D3173; GB:AE000553; GB:AE000511; NID
C;Superfamily: biotin carboxylase; biotin carboxylase homology
F;18-458/Domain: biotin carboxylase homology <BCH>
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| : | : | : | : | : | : | WALMSDKSKAKSVMKEAGMPVIEGSDGLLKS------YQEA------E 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSRILIANRGEIALRAIQTIQEMGKES------IAIYSIADKDAHYLNTASAKVC 64
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                                                                    SIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84;
                                                                                                   Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.8%; Score 662; DB 2; Length 45: 32.1%; Pred. No. 2.2e-39; ive 86; Mismatches 179; Indels
                                                                                                                                                                                                                                             biotin carboxylase - Helicobacter pylori (strain 26695)
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Best Local Similarity 32.1%
Matches 165, Conservative
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acetyl-CoA carboxylase biotin carboxylase subunit accC [imported] - Bacillus halodurani
C,Species: Bacillus halodurans
C,Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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R;Takani, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Norleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83998
A;Status: preliminary
108 AMGHALDAFEVEG-IGHNLPFLSAVMDHPRFREGALTTAFI 447
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propionyl-CoA carboxylase (EC 6.4.1.3) [imported] - Brucella melitensis (strain 16M)

RESULT 36

451

-----NGWAIESRLYAEDPYRNFLPSIG 353

13,

105

141

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154

47 94

330

201

319

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-667 <KUR>
A;Cross-references: UNIPROT:Q8U9Z4; UNIPARC:UP1000016442C; GB:AE007870; PIDN:AAK89816...
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.Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein AGR L. 580GM [imported] - Agrobacterium tumefaciens (strain C58, C; Species: Agrobacterium tumefaciens C; Species: 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 31-Dec-2004 C; Accession: F98286 R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001 A; Title: Genome Sequence of the plant Pathogen and Biotechnology Agent Agrobacterium A; Reference number: A97359; MUID:21608551; PMID:11743194
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                                                                                                                                                                                                                                                                        155 PGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAE 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 YSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGM 450
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                                                                                                                                                                                                                                                                                                                                                                                                      APLLAAKQIGYPVLLKASAGGGGRGQKVIRTQEELQKGFNQAQEEARLYFGDPAIIMEKF
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                                                                                                                        ----VLLADE
                                                                                                                                                                         95 YVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGP
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                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
     Pred. No. 3.8e-39;
1; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.6%; Score 656.5; DB 2; 31.1%; Pred. No. 9.6e-39; ive 95; Mismatches 185;
                                                                                                                                                                                                                                                                                                                      106 TPESMRALGSKAGGREIAAQSNVPTVP--GTGVLESV---
                                                                                                      LKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 NIQODDVKLH------
     l Similarity 31.0%; Pr
160; Conservative 98;
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Matches 170; Conservative 9
Best Local Similarity
Matches 160; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B7558
R;Mhite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                NIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:AE001874; GB:AE000513; NIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acetyl-CoA carboxylase, biotin carboxylase subunit - Deinococcus radiodurans (strain R1)
A; Molecule type: DNA
A; Residues: 1-52 < CAD.
A; Residues: 1-52 < CAD.
A; Cross-treferences: UNIPROT: 09K963; UNIPARC: UP100000C3FE1; GB: AP001516; GB: BA000004; 1
A; Experimental source: strain C-125
C; Genetics:
A; Gene: acc
C; Superfamily: biotin carboxylase; biotin carboxylase homology
                                                                                                                                                                                                                                                    11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 DFRHVEIQVLADNHGHVIHLGERDCSIQRRLQXLLEETPSPAITEKKKKEMGEAAVAAAK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 LVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYS 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 IRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMGA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 LTE-----LNFRSSTSTW-GYFSVGTSGALHEYADSQFGHIFAYGADRSEARKOMVISL 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 LKSYLAPGGLGVRVDSAAYPGY-----TIPPFYDSMIAKVITHGATRDEALAKMKRAL 408
                                                                                                                                                                                                                                                                                                                                                                                                                                               50 CIGPTPSAKSYLNFTNIMSVATLTEVDAIHPGYGFLAENADFAE--ICGECNITFVGPSA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----EGIIESVEDG 144
                                                                                                                                                                                                                                                                                                                                 EVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 SAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETWMSDQGFLTVSDDVYQQACIHTAEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVP---GSP-VFVMKLAG
                                                                                                                                                                                                                                                                                             37 VITKVLICNNGIAAVKEIRSIRKMAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAK
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                                                                                                                                                                                                                                              84;
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                                                                                                                                                                                                Length 452;
                                                                                                                                                                                           ; Score 660; DB 2; Length 45; Pred. No. 3e-39; 82; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 AEFEVEG-IETTIPFHLRLLNHETFVSGDFNTKFLE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: biotin carboxylase; biotin carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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                                                                                                                                                                                              22.7%;
32.8%;
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                                                                                                                                                                                        Query Match 22.7%
Best Local Similarity 32.8%
Matches 169, Conservative
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A; Residues: 1-445 <WHI>
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QY         217 LEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKOLYNAVLGEVPGSPVFVMKLAG         272           IS	Search completed: Pebruary 4, 2006, 18:13:41 Job time : 50 secs	
157 SAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETWMSDQGFLTVSDDVYQQACIHTAEEG 216	Db 468 LSAIAAI 474	RESULT 40 hypothetical protein peca [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C.Species: Agrobacterium tumefaciens C.Species: Agrobacterium tumefaciens C.Species: Agrobacterium tumefaciens C.Species: Agrobacterium tumefaciens C.Species: Agrobacterium tumefaciens C.Species: Agrobacterium tumefaciens C.Species: Agrobacy C.Species: Agrobacy C.Species: Agrobacy C.Species: Agrobacy C.Species: Agrobacy C.Species: Agrobacy C.Species: Agrobacy C.Species: Agrobacy C.Species: Agrobacy C.Stence 294, 2317-2332, 2001 A, Authories: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreepan, W.; Perry, M.; McClell Science 294, 2317-2332, 2001 A, Authories: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreepan, W.; Perry, M.; Gordon-Kamm, A; Reference number: AB2577; MulD: 21608550; PMID: 11143193 A, Accession: AG2997 A, Sterus: preliminary A, Nolecule: Agrobacterium tumefaciens C58. A, Specimen ago, A, Gross-references: UNIPROT: 081924; UNIPARC: UP10000002267; GB:AE008689; PIDN: AAL44393.1; A, Rolecule: Agrobacterium tume acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C, Generium tuma acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-C, Superfamily: human acetyl-CoA carboxylase; biotin carboxylase; biotin carboxylase; biotin carboxylase; biotin carboxylase; biotin carboxylase; biotin carbox

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Sequence 119, App
Sequence 118, App
Sequence 3, Appli
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                                                                                       ; Search time 50 Seconds (without alignments) 924.314 Million cell updates/sec
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2907
1 PPPDHKAVSQFIGGNPLETA..........LDGLIQDRLTAERPPADLAV 559
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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.09-839-477-8
.09-248-796A-17027
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                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .08-611-107-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-611-107-31
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                                                                                                                                                                                                                                                              572060 seqs, 82675679 residues
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                                                                                        4, 2006, 18:13:07
                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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    protein search,

                                                                                          February
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                                                           OM protein
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17494, 7	Sequence	US-09-248-796A-17494	~	1085	22.8	663	45
6725, Ap	Sequence	US-09-328-352-6725	~	670	22.9	667	44
121, App	Seguence	US-09-433-043B-121	7	453	23.4	679.5	43
	Sequence	US-09-433-043B-6	7	453	23.4	679.5	42
6, Appli	Seguence	US-08-475-879-6	-	453	23.4	679.5	. 41
6, Appli	Seguence	US-08-485-607-6	н	453	23.4	679.5	40
6, Appli	Sequence	US-08-476-537-6	Н	453	23.4	679.5	33
6, Appli	Sequence	US-07-956-700B-6	Н	453	23.4	679.5	38
8, Appli	Sequence	US-08-468-793-8	N	453	23.4	681.5	37
8, Appli	Sequence	US-08-422-560A-8	٦	453	23.4	681.5	36
8, Appli	Sequence	US-08-611-107-8	Н	453	23.4	681.5	35
122, App	Sequence	US-09-433-043B-122	~	593	24.4	709.5	34
6, Appli	Sequence	UŞ-08-468-793-6	7	447	24.4	709.5	33
6, Appli	Sequence	US-08-422-560A-6	Н	447	24.4	709.5	32
6, Appli	Sequence	US-08-611-107-6	Н	447	24.4	709.5	31
117, App	Sequence	US-09-433-043B-117	~	491	33.1	961.5	30
	Sequence	US-09-433-043B-109	7	491	33.1	963.5	53
109, App	Sequence	US-08-475-879-109	Н	491	33.1	963.5	28

## ALIGNMENTS

129 WGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIK 188 70 SHFLGGNSVLNAEPSKVRDFVRAHQGHTVISKILLIANNGIAAVKEIRSVRKMAYETFGDE 9 SQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDE 69 RAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAG 189 ETWMSDQ-GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGE APPLICANT: Graham Keith DIXON
APPLICANT: John Leslie THAIN
APPLICANT: John Leslie THAIN
APPLICANT: John Philip VINCENT
APPLICANT: John Philip VINCENT
APPLICANT: Suberna Jini CHAVDA
TITLE OF INVENTION: Acetyl-CoA-Carboxylase from Candida Albicans
TITLE OF INVENTION: Acetyl-CoA-Carboxylase from Candida Albicans
FILE REFERENCE: 009901/0270671 - PRF/PHM70303/UST
CURRENT APPLICATION NUMBER: US/09/581,909
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1997-12-20
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 3
IENGTH: 2270 DB 2; Length 2270; 1; Indels 70.9%; Score 2061.5; DB 2; 70.7%; Pred. No. 2e-179; iive 63; Mismatches 98; Sequence 3, Application US/09581909 Patent No. 6566048 GENERAL INFORMATION: TYPE: PRT ORGANISM: Candida albicans Best Local Similarity 70.7 Matches 390; Conservative -09-581-909-3 US-09-581-909-3 Query Match RESULT 1 g g 셤 8 ò ò

129 128 189

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247

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308 EEAPVIIAPEDARESMEKAAVRLAKUVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHP 367

248 EFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKII

307

250 EVKIDPQTNLVSVADDIYAKGCCTSPEDGLEKAKKIGFPVMIKASEGGGGKGIRKVDDEK 309

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                      361 RLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESF 420
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                                                                                                                              443 KKORRPIPKGHCTACRITSEDPNDGFKPSGGTLHELNFRSSSNVWGYFSVGNNGNIHSFS
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                                              383 RLQVEHPTTEMVSGVNLPAAQLQ1AMGIPMHRISDIRTLYGMNPHSASEIDFEFKTQDAT
                                                                                                      KTQRKPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA
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APPLICATION NUMBER: US/08/354,973
FILING DATE: 13-DEC-1994
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llarity 69.1%; Pred. No. 2.7e-179;
Conservative 76; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Ciba-Geigy Corporation
STREET: Patent Dept., 520 White Plains Rd.,
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF/5-19802/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Vahlensieck, Hans-Friedrich
APPLICANT: Hinnen, Albert
TITLE OF INVENTION: Fungi Resistant to
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
                                                                                                                                                                                                                                                                            DGLIQDRLTAERPPADLAV 559
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| S63 DDLITHKWTAEKPDPTLAV 581
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Patent No. 5641666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary
REGISTRATION NUMBER: 40,403
REFRENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity
Matches 386; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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HYPOTHETICAL:
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                                                                                                                                                                                                                                  SGTGIKETMMSDQ--GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 RRHOKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ACCD:338 BUGS
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
FRIOR APPLICATION NUMBER: 08/475,879
FRIOR PLING DATE: 1995-06-07
FRIOR PLING DATE: 1995-06-07
FRIOR PRICATING DATE: 1995-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 120
370. BEAPUTIARKETFHEMENAAVRLGKLVGYVSAGTVEYLYSHAEDKFYFLELNPRLQVEHP
                                                                                                                                                POGHVVACRITAENPDIGFKPGMGALTELNFRSSISTWGYFSVGISGALHEYADSQFGHI
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US-09-433-0438-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.9%; Score 2060; DB 2; Length 802; 69.1%; Pred. No. 5.4e-180; ive 76; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 120, Application US/09433043B
Patent No. 6399342
GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                    548 LTAERPPADLAV 559
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Best Local S:
Matches 386
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340 EVPGSPIFVWRLAKQSRHLEVQILADQYGNAISLFGRDCSVQRRHQKIIEEAPASIATSV 399
                         TVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLG 258
                                                                                                                                                                                                                                                    AAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRIT 438
                                                                                                                                                                                                                                                                                                                           439 AENPDIGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498
                                                                                                                                                                                                                                                                                                                                                                                                        499 KQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLA 558
                                                                                                                                                                                                                                                                                                                                                                                                                                82 LKVNADYIR-MADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPE 140
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                                                                                                                                                                         319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEPAFLELNPRLQVEHPTTEMVSGVNIP
                                                                                                                                                                                                 400 VFEHMEQCAVKLAKAVGYVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPCTEMYADVNLP
                                                                                                                                                                                                                                                                          102 ASP-ABEVTREGGNKVIEKVLIANNGIAAVKCMRSIRRWSYEMFRNERAIRFVVMVTPED
                                                                                                                                                                                                                                                                                                                                                   SENPDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFADSQFGHCFSWGENREEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 SLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 LLL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSGSGLRVDWQENDFSKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
TITLIGANT: SORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:3380E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.7%; Score 1765.5; DB 2; Best Local Similarity 63.3%; Pred. No. 6.5e-153; Matches 343; Conservative 80; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/433,043B CURRENT FILING DATE: 1999-10-25 PRIOR APPLICATION NUMBER: 08/475,879 PRIOR FILING DATE: 1995-06-07 PRIOR APPLICATION NUMBER: 07/956,700 PRIOR PILING DATE: 1992-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 118, Application US/09433043B Patent No. 6399342 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver. 2
SEQ ID NO 118
LENGTH: 852
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                                                                              DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL 540
                                                                                                                                  RKCTNGEEFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQ 300
                                                                                                                                                                                                             RRHOKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 360
                                                                                                                                                                                                                                                                                      RLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESF 420
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SGTGIKETMMSDQ--GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGI
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TITLE OF INVENTION: CRANGBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REPERENCE: ARCD: 33803
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/956,700
PRIOR PILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
SOFTHARE: PATENTIN VE: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Peptide
US-09-433-043B-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 119, Application US/09433043B
Patent No. 6393342
GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
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63.4%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 63.4%
Matches 343; Conservative
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US-09-433-043B-119
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                                                                                                                                                                                                TFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVH 123
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APPLICANT: Sceller, Kaith R.
APPLICANT: Shorrosh, Basil S.
TITLE OF INVENTION: Structure and Expression of an
TITLE OF INVENTION: Arabidopsis Acetyl-coenzyme A Carboxylase Gene
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEB: Harness ning.
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         Mismatches
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CITY: Bloomfield Hills
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,630
FILING DATE:
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      97;
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CURRENT APPLICATION DA
APPLICATION NUMBER:
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         301;
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339 AEVPGSPIFVWRLAKQSRHLEVQILADQYGNAISLFGRDCSVQRRHQKITEEAPAAIATP 398
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Patent No. 5925805
GENERAL INFORMATION:
APPLICANT: Ohlrogge, John B.
APPLICANT: Roesler, Keith R.
APPLICANT: Shorrosh, Basil S.
TITLE OF INVENTION: Structure and Expression of an TITLE OF INVENTION: Arabidopsis Acetyl-coenzyme A Carboxylase Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1578; DB 1; Length 2254; Pred. No. 4.8e-135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 'IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRETT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,010
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, Dealn F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 655
TELECOMMUNICATION INFORMATION:
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F: P.O. Box 828
Bloomfield Hills
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: ADDRESSEE: Harness, I
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STRANDEDNESS: un
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STATE: Michigan
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGIKETWMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQ 363
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                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                ; DB 1; Length 2254; 4.8e-135;
                                                                                                                                                                                                                                            54.3%; Score 1578; DB 1; Length 2
53.3%; Pred. No. 4.8e-135;
.ive 97; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09839477
Patent No. 6723895
GENERAL INFORMATION:
APPLICANT: Shorrosh, Basil S.
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS CONTAINING A CYTOSOLIC ACETYL
TITLE OF INVENTION: COA-CARBOXYLASE
FILE REFERENCE: 01148-094001
CURRENT APPLICATION NUMBER: US/09/839,477
CURRENT FILING DATE: 2001-04-20
                                     REFERENCE DOCKET NUMBER: 6550-00002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
TELEPAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2254 amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            Query Match 54.3
Best Local Similarity 53.3
Matches 301; Conservative
                                                                                                                                                                     unknown
                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-790-519-3
                                                                                                                                                                                  unknown
                                                                                                                                                  amino acid
                                                                                                                                                                  STRANDEDNESS:
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US-09-839-477-8
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
RIOR FILING DATE: 1998-08-13
SEQ ID NOS: 28208
SEQ ID NOS: 28208
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                                                                                                                                                                                                                      Length 2257;
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                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                   54.3%; Score 1577.5; DB 2;
llarity 54.3%; Pred. No. 5.3e-135;
Conservative 93; Mismatches 139;
PRIOR APPLICATION NUMBER: US 60/198,794
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 12
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 2257
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                                                                                                                                                 ; ORGANISM: Medicago sativa
US-09-839-477-8
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551 ERPPWYLSV 559
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Matches 298; Conserv
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US-09-248-796A-17027
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                                                                                                                               TYPE: PRT
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ADDRESSEE:
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                                                                                                                     101 GSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMR 160
                                                                                                                                                                                  SLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQ-GFLTVSDDVYQQACIHTAEEGLEK 219
                                                                                                                                                                                                74 SLGDKISSTIVAQHAQVPCIPWSGTGVDEVKIDPQTNLVSVADDIYAKGCCTSPEDGLEK 133
                                                                                                                                                                                                                                                                                                         QLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSA 339
                                                                                                                                                                                                                                                                                                                         254 GTVEYLYSHAEDKFYFLELNPRLQVEHPTTEMVTGVNLPAAQLQIAMGIPMHRIRDIRTL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVE 519
                                                                                                                                                                                                                                             AEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEV 279
                                                                                                                                                                                                                                                                          134 AKKIGFPVMIKASEGGGGKGIRKVDDEKNFITLÝNQAANEIPGSPIFIMKLAGDARHLEV 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                  YGMDPRGNEVIDPDFSSPESFKTQRKPQPGGHVVACRITAENPDTGFKPGMGALTELNFR 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                     73
                                                                                                                                        14 GTININIYANVDLIVEIAESTINAHAVWAGWGHASENPLLPEKLAASPKKIIFIGPPGSAMR
                                                             DB 2; Length 442;
                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEIC ACID COMPOSITIONS ENCODING
ACETYL-COA CARBOXYLASE AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 15/08/611,107 FILING DATE: CONCURRENTLY Herewith
                                                                      2.3e-135
                                                        54.0%; Score 1569.5; 70.2%; Pred. No. 2.3e;ive 49; Mismatches
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APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-0C-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/09340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 08/422,560
FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5801233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30-SEP-1993
           ; ORGANISM: Candida albicans
US-09-248-796A-17027
                                                                        Similarity 70.2
95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gornicki, Pio
TITLE OF INVENTION: NUCL
TITLE OF INVENTION: THER
TITLE OF INVENTION: THER
CUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, Whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.O. Box 4433
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STREET: P.C.
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                                                                                     295;
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                                                        Query Match
Best Local S
Matches 295
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TYPE: PRT
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320 RESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPA 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 --MEKGIIFLGPPSAAMGALGDKIGSSLIAQAAGVPTLPWSGSHVKVPQETCHS----- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 VSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGE 259
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Patent No. 5910626
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-CA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS FOR USE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.8%; Score 1565; DB 1;
Best Local Similarity 54.6%; Pred. No. 7.5e-134;
Matches 300; Conservative 91; Mismatches 132;
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTATION NUMBER: 33,928
REFERRINCE/DOCKET NUMBER: ARCD:221
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                                      ; TYPE: amino acid; STRANDEDNESS: TOPOLOGY: linear US-08-611-107-10
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ERPPWYLSV
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200 VSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGGGGIRKCTNGEEFKQLYNAVLGE 259
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,793
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US 08/422,560
FILING APPLICATION NUMBER: US 08/422,560
FILING DATE: 14-APR-1995
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
CLASSIFICATION NUMBER: PCT/US93/09340
FILING DATE: 30-SEP-1993
CLASSIFICATION NUMBER: PCT/US93/09340
FILING DATE: 30-SEP-1993
CLASSIFICATION NUMBER: 33-28
REGISTRATION NUMBER: 33-28
REGISTRATION NUMBER: 33-928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELEPHONE: (512) 418-300
TELEPHONE: (512) 418-300
TELEBAS: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 53.8%; Score 1565; DB 2; Best Local Similarity 54.6%; Pred. No. 7.5e-134; Matches 300; Conservative 91; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                   y sequence 10, Application US/08468793
; Patent No. 6177267
; GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-COA CARBON
; TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold whir
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States of America
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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538 ERPPWYLSV 546
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STRANDEDNESS: Bil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 IPEEIYKNACVSTTDEAVASCQVVGYPAMIKASWGGGGKGIRKVHNDDEVRALFKQVQGE 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.8%; Score 1565; DB 1; Length 2
54.6%; Pred. No. 7.5e-134;
tive 91; Mismatches 132; Indels
                                                                                                                                                                                                                                     SOFTWARE PATENTING STATES:

SOFTWARE PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,560A
FILING DATE: 14-APR-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/956,700
FILING DATE: 02-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REGISTRATION NUMBER: 37,259
REGISTRATION NUMBER: 37,259
REGISTRATION NUMBER: 31,259
REGISTRATION NUMBER: 31,259
REGISTRATION NUMBER: 31,259
RELERAN: 512-418-3000
TELLERAN: 512-418-3000
TELLERAN: 512-418-3000
SEQUENCE CHARACTERISTICS:
LEGISTRATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LEGISTRATION SOLID NO: 10:
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LEGISTRATION S
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                    STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Flogpy d
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Best Local Similarity
Matches 300; Conserva
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US-08-422-560A-10
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Gaps

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Length 2257;

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Local Similarity
                  294;
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184 IPEEIYKNACVSTIDEAVASCQVVGYPAMIKASWGGGGKGIRKVHNDDEVRALFKQVQGE 243
                            VPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDA 319
                                                 244 VPGSPIFIMKVASQSRHLEVQLLCDKHGNVAALHSRDCSVQRRHQKIIEEGPITVAPPET 303
                                                                                  320 RESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPA 379
                                                                                                  AQLQVAMGIPLYSIRDIRILYGMDPRGN------EVIDFDFSSPESFKTQRKPQPQG 430
                                                                                                                                                       SQVVVGMGIPLYNIPEIRRFYGIEHGGGYHAWKEISAVATKFDLDKAQSVK-----PKG 417
                                                                                                                                                                                             HVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAY 490
                                                                                                                                                                                                             491 GADRSEARKOMVISLKELSIRGDFRITVEYLIKLLETDAFESNKITTGWLDGLIQDRLTA 550
                                                                                                                                                                                                                                                                  APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Plotr
TITLE OF INVENTION: Methods for Detecting Nucleic Acid
TITLE OF INVENTION: Segments Encoding Acetyl-Coa Carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino Acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/934,386
FILING DATE: 19-SEP-1997
TITORNOW. A35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08934386 Patent No. 6306636 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: one-of(291, 316, OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.O. Box 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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Length 2311;

DB 2;

Score 1547.5;

53.2%;

Query Match

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METHODS AND AN ACETYL COA CARBOXYLASE GENE
FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN
OIL CONTENT OF PLANTS
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                                                                                               407 RETVKELEQAARRLAKAVGYVGAATVEYLYSMETGEYYFLELNPRLQVEHPVTEWIAEVN
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                           Gaps
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PatentIn Release #1.0, Version #1:30 (EPO)
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  Pred. No. 3.1e-132;
5; Mismatches 140;
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Patent No. 6069298
GENERAL INFORMATION:
                       95;
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53.5%;
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Best Local Similarity 53.5'
Matches 294; Conservative
                           Conservative
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APPLICATION NUMBER: US
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHATILE OF INVENTION: FOR TITLE OF INVENTION: OIL NUMBER OF SEQUENCES: 11 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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AERPPWYISV
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STRANDEDNESS: si
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RESULT 16
US-08-930-285-6
; Sequence 6, Application US/08930285
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                                                                                                                                                                                                                                       257 LGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIERAPVTIAP 316
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                                                                                                                                    EDLKVNADY I RMADQYVEVPGGSNNNNYANVDL I VDVAERAGVHAVWAGWGHASENPRLP
APASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHOD FOR PRODUCING PLANT ACETYL COANUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, STREET: P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,651
FILING DATE: 12-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-695-651-6
Sequence 6, Application US/08695651
Patent No. 6146867
GENERAL INFORMATION:
APPLICANT: Gengenbach, B. G.
APPLICANT: Somers, D. A.
APPLICANT: Wyse, D. L.
APPLICANT: Bgli, M. A.
APPLICANT: Egli, M. A.
APPLICANT: LOLORY: S. M.
APPLICANT: LULZ. S. M.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/417089
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PARFERO ...
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AERPPWYISV 652
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                 APPLICATION NUMBER: 08/014326
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917462
FILING DATE: 21-JUL-1992
APPLICATION NUMBER: 07/538674
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INPORMATION:
NAME: WOSSENEY, WAITEN D
REGISTRATION NUMBER: 30,440
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
TELEFRENCE: 600.318
TELEFAK: 612-339-3061
05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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643 AERPPWYISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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APPLICANT: Wyse, D. L.
APPLICANT: Gromwald, J. W.
APPLICANT: Gromwald, J. W.
APPLICANT: BG11, M. A.
APPLICANT: Lutz, S. M.
APPLICANT: Lutz, S. M.
TITLE OF INVENTION: METHODS AND AN ACETYL COA CARBOXYLASE GENE
TITLE OF INVENTION: FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN OIL
NUMBER OF SEQUENCES: 11
                        430 GHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFA 489
                                                                                                             377 IPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFD-----FSSPESFKTQRKPQPQ 429
                                                                                                                                                                  YGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: PSECESOV VOEFSION 2.0
SURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/695,421
FILING DATE: 23-AUG-1996
CLASSIPICATION B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/417089
FILING DATE: 05-APR-1995
APPLICATION NUMBER: 08/101426
FILING DATE: 21-UL-1992
APPLICATION NUMBER: 07/917462
FILING DATE: 21-UL-1992
APPLICATION NUMBER: 07/53674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-JUN-1990
FILING AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08695421
Patent No. 6268550
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REPERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELECOMMUNICATION INFORMATION TELEPHONE: 612-373-6900
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IBM Compatible
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N-terminal
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643 AERPPWYISV 652
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STRANDEDNESS: si
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FRAGMENT TYPE:
-08-695-421-6
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      GENERAL INFORMATION:
APPLICANT: Regents of the University of Minnesota, et al.
TILLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ACETYL COA CARBOXYLASE GE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 --AIPEEMYRKACVITITEEAVASCOVVGYPAMIKASWGGGGKGIRKVHNDDEVRALFKOV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 QGEVPGSPIFVMRLASQSRHLEVQLLCDQYGNVAALHSRDCSVQRRHQKIIEEGPVTVAP 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 EDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 ESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIK---ETMMSDQG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 FLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 LGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAP 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                      ADDRESSEE: Schwegman, Lundberg, Woesener & Kluth, P. A. STREET: P. O. Box 2938
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                            SOUTWARE: Past.Edu.
SUCTYARE: Past.Edu.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,285
FILING DATE: 13-APR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04625
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Embretson, Janet E.
REGISTRATION NUMBER: 39,665
REFERENCE/DOCKET NUMBER: 600.318US4
TELECHONICATION INFORMATION:
TELECHONICATION INFORMATION:
TELECHONICATION INFORMATION:
TELECHONICATION INFORMATION:
TELECHONICATION INFORMATION:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 2325 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
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FastSEQ Version 2.0 CATION DATA:
                                                                                                                                                                                                                                                                          2325 amino acide
                                                                                                                                                                                                     TELEPHONE: 612-359-3260
TELEFAX: 612-359-3263
                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550 AERPPADLAV 559
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                                                                                                                         EDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLF 139
                                                                                                                                                                            140 ESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIK---ETMMSDQG 196
                                                                                                                                                                                          197 FLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAV 256
                                                                                                                                                                                                                                                                                       LGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAP 316
                                                                                                                                                                                                                                                                                                      QGEVPGSPIFVMRLASQSRHLEVQLLCDQYGNVAALHSRDCSVQRRHQXIIEEGPVTVAP 406
                                                                                                                                                                                                                                                                                                                                              EDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVN 376
                                                                                                                                                                                                                                                                                                                                                            IPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFD-----FSSPESFKTQRKPQPQ 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLT 549
                                                                                                                                     APASPVADFIRKOGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATP
                                       21;
               Length 2325
              53.1%; Score 1543.5; DB 2; Length 53.5%; Pred. No. 7.4e-132; ive 94; Mismatches 141; Indels
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APPLICANT: Somers, D. A.
APPLICANT: Egli, M. A.
APPLICANT: Wyse, D. L.
APPLICANT: Wyse, D. L.
APPLICANT: Wyse, D. L.
APPLICANT: Van Dee, K. L.
APPLICANT: Van Dee, K. L.
APPLICANT: Parker, W. B.
TITLE OF INVENTION: GENE COMBINATIONS FOR HERBICIDE TITLE OF INVENTION: TOLLERANCE IN CORN NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
US-08-697-826A-10
; Sequence 10, Application US/08697826A
; Patent No. 6414222
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IBM Compatible
            Query Match
Best Local Similarity 53.5
Matches 294; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATING SYSTEM: DOS
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AERPPWYISV 652
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377 IPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFD-----FSSPESFKTQRKPQPQ 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 ESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIK---ETMMSDQG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 --AIPEEMYRKACVTTTEEAVASCQVVGYPAMIKASWGGGGKGIRKVHNDDEVRALFKQV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 QGEVPGSPIFVWRLASQSRHLEVQLLCDQYGNVAALHSRDCSVQRRHQKIIEEGPVTVAP 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 EDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVN 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 ASVSKVVBFCAALGGKTPIHSILVANNGMAAAKFWRSVRTWANDTFGSEKAIQLIAMATP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 FLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 LGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAP 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 APASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.1%; Score 1543.5; DB 2; Best Local Similarity 53.5%; Pred. No. 7.4e-132; Matches, 294; Conservative 94; Mismatches 141;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,826A
FILING DATE: 29-AUG-1997
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: PCT/US96/04625
FILING DATE: 04-APR-1996
FILING DATE: 30-AUG-1996
ATTORNEY/ACENT INFORMATION:
NAME: WOOSSHOEY, WATTEN D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 30,440
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
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                                                                                              374 GVNIPAAQLQVAMGIPLYSIRDIRTLYGM-DPRGNEVIDFDFSSPESFKTQRKPQPQGHV
                                                                                                                                                                                            493 DRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIODRLTAER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENE THAT ENCODES ACETYL-COENZYME A CARBOXYLASE FROM CYCLOTELLA CRYPTICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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FILING DATE: April 7, 1995
CLASSIFICATION: 800
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/104,938
FILING DATE: September 14, 1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: O'CONNOR, EDNA
REGISTRATION NUMBER: 29,252
REGISTRATION NUMBER: MRI/NREL IR# 92-48CON
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GENE THAT ENCODES ACETYL-COENTITLE OF INVENTION: CARBOXYLASE FROM CYCLOTELLA CINTMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NATIONAL RENEWABLE ENERGY LABORATORY
STREET: 1617 Cole Blvd.
CITY: Golden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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95; Mismatches 140;
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53.2%; Pred. No. 3.6e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/08418893D Patent No. 5559220 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ROESSLER, PAUL G
APPLICANT: OHLROGGE, JOHN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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Best Local Similarity 53.2
Matches 291, Conservative
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MEDIUM TYPE: Floppy
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STRANDEDNESS: Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGT-----GIKETMMSDQ 195
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                                                                                                                                    GENE THAT ENCODES ACETYL-COENZYME A CARBOXYLASE FROM CYCLOTELLA CRYPTICA
                                                                                                                                                                                                          ADDRESSEE: NATIONAL RENEWABLE ENERGY LABORATORY STREET: 1617 Cole Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/08/418, 893D
FILING DATE: April 7, 1995
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53.2%; Pred. No. 3.6e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 800
PRIOR APPLICATION NUMBER: US 08/104,938
FILING DATE: September 14, 1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: O'CONNOR, EDNA
REGISTRATION NUMBER: 29,252
REFERENCE/DOCKET NUMBER: MRI/NREL IF
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
                   Sequence 23, Application US/08418893D Patent No. 5559220 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                      APPLICANT: ROESSLER, PAUL G
APPLICANT: OHLROGGE, JOHN B
TITLE OF INVENTION: CARBOXYLAX
TITLE OF INVENTION: CARBOXYLAX
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSSE: NATIONAL RENEWABI
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                                                                                                                                                                                                                                                                                                                                             ZIP: 80401-3393
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS: siz
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Matches 284; Conservative
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Best Local Similarity
                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                               LENGTH:
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APPLICANT:
APPLICANT:
APPLICANT:
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81 AKSVEDYVKSRGGNRVIRKVLIANNGMAATKSILSMRQWAYMEFGDERAIQFVAMATPED 140
                                                     201 L--DKLGIKFIGPTGPVMSVLGDKIAANILAQTAKVPSIPWSGSFGGPDDGPLQADLTEE 258
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                                                                                                                                                  196 GFLTVSDDVYQQACIHTAEBGLEKAEKIGYP--VMIKASEGGGGKGIRKCTNGEEFKQLY 253
                                                                                                                                                                  GVNIPAAQLQVAMGIPLYSIRDIRTLYGM-DPRGNEVIDFDFSSPESFKTQRKPQPQGHV 432
                                                                                                                                                                                                                                                                                                                                        VACRITAENPDIGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGA 492
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                                                                                                                                                                                                     254 NAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVT 313
                                                                                                                                                                                                                                                               314 IAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVS 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/08611107
Patent No. 5801233
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODI
TITLE OF INVENTION: THEREFOR NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
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02-0CT-1992
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APPLICATION NUMBER: US/08/611,107
FILING DATE: Concurrently Herewith
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: U
FILING DATE: 02-OCT-1
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STREET: P
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                                                                  141
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54 IRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 HADVPCMPWSGTGIK---ETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 ASEGGGGKGIRKCINGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 SIFGRDCSVORRHOKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPES 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 MRSIRTWALETFGNEKAILLVAMATPEDLRINAEHIRIADQFLEVPGGTNNNNYANVQLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.4%; Score 1495; DB 1;
54.8%; Pred. No. 1.9e-127;
iive 87; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         522 IKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 VDLINAAEYRENKIHTGWLDSRIAMRVRAERPPWYLSV
US PCT/US93/09340
              FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
PELLING DATE: 14-APR-1995
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REPRENCE/DOCKET NUMBER: ARCD:221
TELECOMMUNICATION INPORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 444-7577
INPORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 74, Application US/09631594
Patent No. 6737237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOHNSON, JENNIFER J
KIRISITS, MICHAEL
FERGUSON, DAVID
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APPLICANT: MCLEOD, RIMA W.
APPLICANT: ROBERTS, CRAIG W.
APPLICANT: ROBERTS, FIONA
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Dorr, Patrick K.
Parkinson, Tanya
Bulawa, Christine Ellen
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Patent No. 6514726
GENERAL INFORMATION:
APPLICANT: Dorr, Patrick K.
APPLICANT: Parkinson, Tanya
APPLICANT: Bulawa, Christine Eller
                                                                                                    MACK, DOUG
SAMUEL, BENJAMIN
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Toxoplasma gondii
                                                     FERGUSON, DAVID
LYONS, RUSSELL
MUI, ERNEST
                                                                                                                                    GORNICKI, PIOTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 49.5
Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              US-09-631-594-76
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                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                      APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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APPLICANT: MACK, DOUG
APPLICANT: SAWDEL, BENJAMIN
APPLICANT: SAWDEL, BENJAMIN
APPLICANT: GORNICKI, PIOTR
APPLICANT: ZUTHER, ELLEN
TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIACNOSTIC REAGENTS, AND VACCINES
TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIACNOSTIC REAGENTS, AND VACCINES
TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIACNOSTIC REAGENTS, AND VACCINES
TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIACNOSTIC REAGENTS, AND VACCINES
FILE REFERENCE: 1933-9096
CURRENT PILING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-27
PRIOR APPLICATION NUMBER: PCT/US97/12497
PRIOR PILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 83
SOCTIMARE: PATENTIN VET: 2.1
SED ID NO 74
LENGTH-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 RSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEV 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMGALTELNF 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

48.7%; Score 1417; DB 2; Length 48

Best Local Similarity 55.2%; Pred. No. 2.7e-121;

Matches 277; Conservative 77; Mismatches 134; Indels
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EYLVQLLEDKDFIENRIDTSWL 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 23
US-09-631-594-76
; Sequence 76, Application US/09631594
; Patent No. 6737237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MCLEOD, RIMA.W.
APPLICANT: ROBERTS, CRAIG W.
APPLICANT: ROBERTS, FIONA
APPLICANT: JOHNSON, JENNIFER J.
APPLICANT: KIRISITS, MICHAEL
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Toxoplasma gondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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APPLICANT: ZUTHEN, ELLEN
TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIAGNOSTIC REAGENTS, AND VACCINES
TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIAGNOSTIC REAGENTS, AND VACCINES
TITLE OF INVENTION: BASED ON UNIQUE APICOMPLEXAN PARASITE COMPONENTS
FILE REPERENCE: 1938-90966
CURRENT APPLICATION NUMBER: US/09/631,594
CURRENT PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 83
SOFTWARE: 1997-07-18
SOFTWARE: PATENTION OF: 2.1
ENGTH: 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 PVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 MVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQG 430
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356 CVGDFNLPAAQLQVAMGILIDDIPDIKA------YLDSAASN-----KPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIBFTVMATPEDLKVNADYIRMADQYVEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 GFLTVSDDVYQQAÇIHT-----AEBGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 QLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 DAYRQVVNEVKGSPVFVMRMVSDCRHLEVQLLADKSGRCVSLGSRDCSIQRRCQKIIEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.5; DB 2; Length 506; 2.3e-107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.5%; Score 1265.5; DB 2;
49.5%; Pred. No. 2.3e-107;
tive 70; Mismatches 143;
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SEQUENCE CHARACTERISTICS
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TITLE OF INVENTION: ASPERGILLUS FUMIGATUS ACETYL COENZYME-A CARBOXYLASE GENES TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF FILE REPERENCE: 06286/107001
CURRENT APPLICATION NUMBER: US/09/475,252
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: US 60/114,580
PRIOR PILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 FKPSSGTWHELNFRSSSNVWGYFSVGTAGGIHSFSDSQFGHIFAYGETRSASRKHMVVAL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 AAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 AAVSLGKLVGYVSAGTVEYLYSHADDKFYFLELNPRLQVEHPTTEMVSGVNLPAAQLQIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 MGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISL 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FIMKLAGNARHLEVQLLADQYGNNISLFGRDCSVQRRHQKIIEEAPVTIAKPATFQAMER 61
                                                                                                                                                                                                                                                                                                                                                                                                                             266 FVMKLAGQARHLEVOLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV 559
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US-07-956-700B-109
; Sequence 109, Application US/07956700B
; Patent No. 5539902
; Patent No. 5539902
; Title OF INVENTION:
; TITLE OF INVENTION: Cyanobaccerial and Plant Acetyl-CoA TITLE OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                    Length 2016;
                                                                                                                                                                                                                                                                                                                                                                                 44; Indels
                                                                                                                                                                                                                                                                                                                                    39.6%; Score 1152; DB 2; 75.2%; Pred. No. 5.2e-96; iive 29; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,700B
FILING DATE: 19921002
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Thomas E. No. 5539092thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-475-252-2
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INFORMATION FOR SEQ ID NO: 1
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                            LENGTH: 2016
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                                                                                                                                                                                                                                                                                                                              15; Gaps
                                                                                                                                                                                                                                                                              Length 491;
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Fatent No. 5756290

GENERAL INFORMATION:
APPLICANT: Robert Haselkorn and Piotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
TITLE OF INVENTION: Carboxylase
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDERSS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5756290th Clark Street
CITY: Chicago
CITY: Chicago
STRATE: 11linois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                           89;
                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                 ; NAME/KEY: Xaa
; LOCATION: 248, 267, 311, 412, 418, 422, 436,
; IDENTIFICATION METHOD: Xaa = any amino acid
US-07-956-700B-109
                                                                                                                                                                                                                                                                         Query Match 33.1%; Score 963.5; DB 1 Best Local Similarity 54.7%; Pred. No. 1.2e-79; Matches 187; Conservative 51; Mismatches 89
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,537
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APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas B. No. 5756290thrup
REGISTRATION NUMBER: 33,268
LENGTH: 491 amino acids
TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
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347 SPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 491;
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Patent No. 5972644

Patent No. 5972644 5786170

GENERAL INFORMATION:
APPLICANT: Robert Haselkorn and Piotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
ITTLE OF INVENTION: Carboxylase
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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321 No. 5972644 5786170th Clark Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . LOCATION: 248, 267, 311, 412, 418, 422, 436, i IDENTIFICATION METHOD: Xaa = any amino acid US-08-485-607-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Mismatches
                                  NAME: Thomas E. No. 5792627thrup REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,879
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COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 LENGTH: 491 amino acids
TYPE: Amino acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS LENGTH: 491 amino acic
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
MOLECULE TYPE: Peptide
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MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
33.1%; Score 963.5; DB 1; Length 491;
Best Local Similarity 54.7%; Pred. No. 1.2e-79;
Matches 187; Conservative 51; Mismatches 89; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 109, Application US/08485607
Patent No. 5792627
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-COA
TITLE OF INVENTION: Carboxylase
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1, 412, 418, 422, 436, and 474
Xaa = any amino acid
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321 No. 5792627th Clark Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,607
FILING DATE: 07-UN-1995
CLASSIFICATION: 800
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
COMPUTER: PC COMPATIBLE
COMPUTER: PC COMPATIBLE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0690
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 anning acids
                                                                                                                                                                                                                                                                                                                                                                                            311,
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Xaa

LOCATION: 248, 267, 31

LOCATION: AETHOD:

US-08-476-537-109
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APPLICATION NUMBER: 0'
FILING DATE: 10/21/92
                                                                                                                                                                                                                         STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Peptide
                                                                                                                                                                                           TYPE: Amino acid
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 FKSKPNVWAYFSVXSGGAIHEFSDSQFGHVFAXGESRSLALANMVLGLKEIQIRGEIRTN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTT 517
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JATCHEL NINCRMATION:
APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
JITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT APPLICATION NUMBER: US/09/433,043B
FRIOR APPLICATION NUMBER: 09/9-10-25
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
SPRIOR FILING DATE: 1995-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patchlin Ver. 2.1
SEQ ID NO 109
LENGTH: 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.1%; Score 963.5; DB 1; Length 491; 54.7%; Pred. No. 1.2e-79; tive 51; Mismatches 89; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 248, 267, 311, 412, 418, 422, 436, and 474; IDENTIFICATION METHOD: Xaa = any amino acid US-08-475-879-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518 VEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV 559
            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNDRER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5972644 5786170thrup
REGISTATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 29
US-09-433-043B-109
'Sequence 109, Application US/09433043B
'Patent No. 6399342
                                                                                                                                                                                          TELEPHONE: 1-312-744-0090
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino acids
STRANDEDNESS: Single
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.1
Best Local Similarity 54.7
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                      Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GYHAWKEISAVATKFDLDKAQSVK-----PKGHCVAVRVTSEDPDDGFKPTSGRVEELN 234
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APPLICANT: GONDICKY, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:3380S
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT PILING DATE: 1999-10-25
PRIOR PILING DATE: 1999-10-25
PRIOR PELICATION NUMBER: 08/475,879
PRIOR PELICATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 117
LENGTH: 491
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                                                            OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Peptide
NAME/KEY: MOD RES
COCATION: (248)...(474)
OTHER INFORMATION: XAA = Any set containing N
US-09-433-043B-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Peptide
US-09-433-043B-117
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                                                                                                                                                                                                                                         33.1%; Score 963.5; DB; 54.7%; Pred. No. 1.2e-79
                                                                                                                                                                                                                                                                                      51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 117, Application US/09433043B Patent No. 6399342 GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.7%
Matches 187; Conservative
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Pred. No. 2.1e-56;
8; Mismatches 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/956,700 FILING DATE: 02-OCT-1992 ITTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                  88;
  32.9%;
Best Local Similarity 32.9
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wilson, Mark B. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houston
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                        SPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRG 406
                                                                                                181 GYHAWKEISAVATKFDLDKAMSVK-----PKGHCVAVRVTSEDPDDGFKPTSGRVEELN 234
                                                                                                                                                                                                                               FRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKOMVISLKELSIRGDFRTT 517
                                                                                                                                                                                                                                                 287 GNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLY 346
                                                                                                                                                   N-----EVIDEDFSSPESFKTORKPOPOGHVVACRITAENPDTGFKPGMGALTELN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                  518 VEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,107
FILING DATE: CONCURTENTLY Herewith
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US N 07/956,700
FILING DATE: 02-OCT-1992
PRIOR APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US N 08/422,560
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.4%; Score 709.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFRENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08611107
Patent No. 5801233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
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-----GYLPPGGPGVRIDSHVYTDYQIPPYYDSLIGKLIVWGPDRATAINRMKRA 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 YTGAGTIEFLLD-RSGQFYFMEMNTRIQVEHPVTEMVTGVDLLVEQIRIAQGERLRLTQD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 IRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMGALTE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 GGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
                                                                                                                                                                                                                                              54 EPASAKSÝLNIPNIIAAALTRNASAIHPGYGFLSENAKFAEICA--DHHIAFIGPTPEAI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLEVOLLADOYGNAISIFGRDCSVORRHOKIIEEAPVTIAPEDARESMEKAAVRLAKLVG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                456 LNFRSSTSTWGYFSVGTSGA------LHEYADSQFGHIFAYGADRSEARKQMVIS 504
                                                                                                     40 KVLICHNGIAAVKEIRSIRKMAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVP
                                                                                                                                                                                                                                                                                                         160 RSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEV----PGSPVFVMKLAGQAR
Indels 93; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08422560A
Patent No. 5910626
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS FOR USE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,560A
FILING DATE: 14-APR-1995
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276 HLEVOLLADOYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVG 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 447;
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  PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                         FILING DATE: 30-SEP-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: 33,928
TELECOMMUNICATION INFORMATION:
                                                                                                  FILING DATE: 14-APR-1995
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-0CT-1992
CLASSIPTTATION.
                                                                                                                                                                                                         PCT/US93/09340
                                      US/08/468,793
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                                                                                                                                                                                                                                                                                                                                                                              TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERIFICS: LENGTH: 447 amino acids TYPE: amino acid STRANDEDNESS: sincle TOPOLATE
                                                06-JUN-1995
V: 800
                                                                                                                                                                                                                                                                                                                                                                 (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-468-793-6
                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                    FILING DATE: 02-OCT-
CLASSIFICATION: 800
APPLICATION NUMBER:
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APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                   Mismatches 165;
                                                                                                                                                                                                         24.4%; Score 709.5; DB 1
32.9%; Pred. No. 2.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
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Patent No. 6177267
GENERAL INFORMATION:
                                                                                                                                                                                                                                                 88;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
                                                                                        LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS:
                                  TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               Matches 170; Conservative
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CORRESPONDENCE ADDRESS:
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US-08-422-560A-6
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Best Local
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TITLE OF 1
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-----RGHAIECRINAEDPDHDFRPAPGRIS- 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HASELKEN, ROBERT

APPLICANT: GORNICKI, PIOTR

TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE

FILE REFERENCE: ARCD:338US

CURRENT APPLICATION NUMBER: US/09/433,043B

CURRENT APPLICATION NUMBER: US/09/439

PRIOR PILING DATE: 1999-10-25

PRIOR APPLICATION NUMBER: 07/956,700

PRIOR PILING DATE: 1995-06-07

PRIOR PILING DATE: 1992-10-02

NUMBER OF SEQ ID NOS: 128

SOFTWARE: Patentin Ver. 2.1

LENGTH: 593
                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-09-433-043B-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 LKELSIRGDFRITVEYLIKLLETDAFESNKITTGWL 540
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             Sequence 122, Application US/09433043B
Patent No. 6399342
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Patent No. 5801233
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Goznicki, Piotr
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 32.9
Matches 170, Conservative
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                                                   GENERAL INFORMATION:
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160 RSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEK 219
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NUCLEIC ACID COMPOSITIONS ENCODING
ACETYL-COA CARBOXYLASE AND USES
THEREFOR
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.4%; Score 681.5; DB 1; 32.1%; Pred. No. 8e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-58P-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 08/422,560
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/611,107
FILING DATE: Concurrently Herewith
                                                                                                            E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:221
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                             STATE: Texas
COUNTRY: United States of America
ZIP: 77210
                                                                                                                                                                                                                                                            MEDITER REALCHER. Floppy disk COMPUTER: IBM PC compatible COMPOTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEO ID NO: 8: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 32.1%
Matches 168; Conservative
                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                             ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                           INVENTION
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Gornicki, Piotr

us-10-633-835-2.rai

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269 YIGAGTVEFLVD-ATGNPYFMEMNTRIQVEHPVTEMITGLDLIAEQIRIAGG----- 319
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                                                                                                                                              209 HVEFQILADAYGNVVHLGERDCSIQRRHQKLLEEAPSPALSADLRQKMGDAAVKVAQAIG 268
                                                                                                                                                                                                                                           336 YVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRD 395
                                                                                                                                                                                                                                                                                                                                                                                396 IRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMGALTE 455
-------EALRF-----ROADIQLRGHAIECRINAEDPEYNFRPNPGRIT- 357
                                                                                                       276 HLEVOLLADOYGNAISIFGRDCSVORRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 LNFRSSTSTWGYFSVGTSGA------LHEYADSQFGHIFAYGADRSEARKQMVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08468793
Patent No. 6177267
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505 LKELSIRGDFRITVEYLIKLLETDAFESNKITTGWLDGLIQDRL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,793 FILING DATE: 06-JUN-1995 CLASSIFICATION DATE: 06-JUN-1995 GLASSIFICATION NUMBER: US 08/422,560 FILING DATE: 14-APR-1995 APPLICATION NUMBER: US NO 7/956,700 FILING DATE: US-02-OCT-1992 CLASSIFICATION NUMBER: PCT/US93/09340 APPLICATION NUMBER: PCT/US93/09340 FILING DATE: 03-OCT-1993 CLASSIFICATION NUMBER: PCT/US93/09340 APPLICATION NUMBER: PCT/US93/09340 APPLICATION NUMBER: PCT/US93/09340 CLASSIFICATION: 800
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NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
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(713) 789-2679
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MEDIUM TYPE: Floppy disk
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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456 LNFRSSTSTWGYFSVGTSGA------LHEYADSQFGHIFAYGADRSEARKQMVIS 504
                                                                                                                                                                       -----GYLPPGGPGVRVDSHVYTDYEIPPYYDSLIGKLIVWGATREEAIARMQRA 407
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Patent No. 5310626
Patent No. 5310626
PAPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: METHODS:FOR USE
NUMBER OF SEQUENCES: 31
CORRESPONDENCES: 31
ADDRESSE: Arnold, White & Durkee
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                                                                                                                                                                                                                                               505 LKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRL 548
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,560A
FILING DATE: 14 APR-1995
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
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APPLICATION NUMBER: US 07/956,700
FILING DATE: 02-0CT-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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US-08-422-560A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                               269 YIGAGTVEFLVD-ATGNFYFMEMNTRIQVEHPVTEMITGLDLIAEQIRIAQG----- 319
                                                                                                                                                                                                                                                                                                                                                                                   100 GGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 RSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 AEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVP---GSP-VFVMKLAGQAR 275
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                                                                                                     Length 453;
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Patent No. 5539092
GENERAL INFORMATION:
APPLICANT: ROBERT Haselkorn and Piotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
                                                                                                     DB 2;
                                                                                                     23.4%; Score 681.5; DB 32.1%; Pred. No. 8e-54;
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321 No. 5539092th Clark Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,700B
FILING DATE: 19921002
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NAME: Thomas E. No. 5539692thrup
NAGISTRATION NUMBER: 33,268
REPERENCE/DOCKET NUMBER: ARCD:058
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MEDIUM TYPE: Ploppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                       Matches 168; Conservative
   protein
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
STREET: 321 No. 5539
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CLASSIFICATION:
; MOLECULE TYPE:
US-08-468-793-8
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US-07-956-700B-6
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STATE:
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Patent No. 5756290

GENERAL INFORMATION:
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA TITLE OF INVENTION: Carboxylase
NUMBER OF SEQUENCES: 116

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5756290th Clark Street
CITY: Chicago
STREET: 111nois
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MEDIUM TYPE: Floppy bisk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELECOMMUNICATION INFORMATION
TELEPHONE: 1-312-744-0090
TELEPAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                 LENGTH: 453 amino acide
TYPE: Amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                           TOPOLOGY: Linear
MOLECULE TYPE: Peptide
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B: Arnold, White & Durkee
321 No. 5792627th Clark Street
               CORRESPONDENCE ADDRESS ADDRESS: Arnold, 1
                                                                                                                                                                                OPERATING SYSTEM:
                                               STREET: 321 NO. 5
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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/ Sequence 6, Application US/08485607

/ Setent No. 5792637

/ GENERAL INFORMATION:

/ APPLICANT: Robert Haselkorn and Piotr Gornicki

/ TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA

/ TITLE OF INVENTION: Carboxylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                         97; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                      23.4%; Score 679.5; 32.1%; Pred. No. 1.2
                                                              CLASSIPICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5756290thrup
REGISTRATION NUMBER: 33,268
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION: TELECOMMUNICATION:
TELEPHONE: 1-312-744-0090
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,537
                                                                                                                                                                                                                                 TELEPAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    : 453 amino acids
Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                       Single
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear MOLECULE TYPE: Peptide
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Best Local Similarity 32.1%; Pred. No. 1.2e-53;
Matches 168; Conservative 97; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
PRICR APPLICATION DATA:
APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5792627thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,607
FILING DATE: 07-JUN-1995
CTASSIFICATION: 800
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk,
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                ASCII-DOS
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엄

Search completed: February 4, 2006, 18:14:38 Job time : 55 secs

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

4, 2006, 18:05:17; Search time 248 Seconds (without alignments) 1590.284 Million cell updates/sec February Run on:

US-10-633-835-2 2907 1 PPPDHKAVSQFIGGNPLETA........DGLIQDRLTAERPPADLAV 559 Title: Perfect score:

Scoring table: Sequence:

2166443 seqs, 705528306 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

		,			SUMMAKIES		
Result No.	Score	Query Match	Length	DB	ID	Description	. ¤
-	2907	100.0	2185	- 7	O4P5I4 USTMA		ustilago ma
7	2896	9.66	2185	~	O12721 USTMA		ustilago ma
٣	2269		2237	7	QSKFC9_CRYNE		cryptococcu
4	2269	78.1	2237	~	Q55QT6_CRYNE		cryptococcu
S	2190		2288		O60033 EMENI		emericella
9	2190	75.3	28		Q5B004 EMENI		aspergillus
7	2186		2292		Q4X1V2_ASPFU		aspergillus
8	2179	75.0	2275		Q7SBL5 NEUCR	Q7sbl5 neu	neurospora
6	2163	74.4	2344		Q51YC2 MAGGR	-	magnaporthe
10	2148	73.9	2271		Q41878_GIBZE		gibberella
11	2100.5		2231		OCCL34 KLULA		kluyveromyc
12	2090.5		2233		Q6FKK8_CANGA		candida gla
13	2090.5		2280		COAC SCHPO		schizosacch
14	2084		2266		Q6CC91 YARLI		yarrowia li
15	2069.5		2231		Q75EK8 ASHGO		авнруа довв
16	2061.5	70.9	2271		OSAAM4 CANAL		candida alb
17	2060		2233		COAC YEAST		saccharomyc
18	2039.5		2297		Q6BX58_DEBHA		debaryomyce
19	1889.5		2273		HPA1_YEAST		Baccharomyc
20	1889.5	65.0	2273		042823 YEAST		saccharomyc
. 21	1791		2346		Q6XDA8 HUMAN		homo sapien
22	1787	61.5	2346		Q7Z561_HUMAN		homo sapien
23	1785	61.4	2345		COA1 RAT		rattus norv
24	1783.5		2448		Q6JIZ0 MOUSE	_	mus musculu
25	1783		2345		Q5SWU9_MOUSE	QSewn9 mus	musculu
56	1781		2346		COA1_HUMAN	<u>.</u>	homo sapien
27	1780		2323		Q9V346_DROME		drosophila
28	1780	61.2	2324		COAC CHICK		gallus gall
29	1780	•	2482		Q9V347_DROME		drosophila
30	1776	61.1	2345		2	121	
31	1775	61.1	2346	-	COA1_BOVIN	Q9tts3 bos	taurus

	COA1 SHEEP 06KEB9 HUMAN 06KEB9 HUMAN 06TY48 HUMAN 07P011 ANOGA 04SCUJ TETNG 04SCUJ TETNG 05AJ08 DICDI 070151 RAT COA2 HUMAN 06SZP8 PHYIN 06SZP8 PHYIN 06SZP8 PHYIN 06SZP8 BRANA 09FEH8 BRANA	
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Q28559 ovis aries
Q6ke89 homo sapien
Q6ke87 homo sapien
Q6ty48 homo sapien
Q70411 anopheles g
Q4scu3 tetraodon n
Q4su6 tetraodon n
Q4su6 tetraodon n
Q54j08 dictyosteli
O70151 rattus norv
O00763 homo sapien
Q6szp8 phytophthor
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## ALIGNMENTS

USTWA PRELIMINA  2005 (TEEMBLE)  2005 (TEEMBLE)  1103 protein.  1104 protein.  21 protein.  22 protein.  22 protein.  23 protein.  24 protein.  25 protein.  26 protein.  27 p	A 4 4 6 6 6 4 6 6 7 6 7 6 7 6 7 6 7 6 7 6	RESULT 1  Q4P514 USTWA AC Q4P5141 DT Q4P5141 DT 113-SEP- DT 113-SE
	WA TERMINIARY; PRT; 2185 AA.  4 USTRA PRELIMINARY; PRT; 2185 AA.  4 USTRA PRELIMINARY; PRT; 2185 AA.  4 TEMBLEE 31, Last esquence update)  19-2005 (TERMELEE 31, Last esquence update)  19-2005 (TERMELEE 31, Last annotation update)  19-2005 (TERMELEE 31, Last annotation update)  19-2005 (TERMELEE 31, Last annotation update)  19-2005 (TERMELEE 31, Last annotation update)  19-2005 (TERMELEE 31, Last annotation update)  19-2005 (TERMELEE 31, Last annotation update)  19-2005 (TERMELEE 31, Last annotation update)  10-2005 (TERMELEE 31, Last annotation update)  10-2006 (TERMELEE 31, Last annotation update)  10-2006 (TERMELEE 31, Last annotation update)  10-2007 (TERMELEE 31, Last annotation update)  10-2008 (TERMELEE 31, Last annotation update)  10-2008 (TERMELEE 31, Last annotation update)  10-2008 (TERMELEE 31, Last annotation update)  10-2008 (TERMELEE 31, Termelee 31, Last annotation update)  10-2008 (TERMELEE 31, Marcal A1, Mallosen C1, Mallosen C1, Mallosen C1, Mallosen C1, Mallosen C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Schome C1, Whitehea C1, Whitehea C1, Whitehea C2, Whyman D1, Yannok C2, Whyman D1, Yannok C2, Termelee C1, Whitehea C2, Whyman D2, Yannok C2, Termelee C2, Whyman D2, Yannok C2, Termelee C2, Whyman D3, Yannok C2, Whyman D3, Yannok C2, Yannok C2, Yannok C2, Yan	1 USTW USTW USTW USTW USTW USTW USTW USTW

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Matches 55
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Pfam;
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                                                                                                                                                                                     61 AYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERA 120
                                                                                                                                                                                                 GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180
                                                                                                                                                                                                                                                                                                                      RKCTNGEEFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTORKPOPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSQPGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQ 301
                                                                                                                                                                                                                                                                                                                                                                                    RRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP 361
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                                                                                                                                                                                                                                                                                           PWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGGKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTORKPOPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA
                                                                                                                                                                                                                                                                            PWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGI
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                                                                                                                                          1 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKW
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96086936; PubMed=7500941; DOI=10.1007/BF00290366;
Bailey A.M., Keon J.P.R., Owen J., Hargreaves J.A.;
"The ACC1 gene, encoding acetyl-CoA carboxylase, is essential for
                                                                                                                     ò
                                                                                                Length 2185;
e genome sequence of Ustilago maydis.";
nitted (FEB-2004) to the EMBL/GenBank/DBU databases.
CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (MGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fungi, Basidiomycota, Ustilaginomycetes,
Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
NCBI_TaxID=5270;
                                                                                                                    Indels
                                                                          2185 AA; 240063 MW; 8C2ECBF613483DF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
ACETYL COA Carboxylase (EC 6.4.1.2).
                                                                                              100.0%; Score 2907; DB 2;
100.0%; Pred. No. 2.9e-189;
iive 0; Mismatches 0;
                                          preliminary data.
EMEL, AACPO1000168; BAX85486.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 2185 AA; 240063 WW; 8C2ECBF6134831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGLIQDRLTAERPPADLAV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ustilago maydis (Smut fungus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q12721 USTMA PRELIMINARY, Q12721;
                                                                                                         Best Local Similarity 100.
Matches 559; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=IMI103761;
 "The genom
Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGI
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                                                                                                                                                         activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.6%; Score 2896; DB 2; 99.6%; Pred. No. 1.6e-188;
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                                                                                                    P; Q00955; 10D4.
G Q1271; 11-545.
G O1003999; F:acetyl-CoA carboxylase
GO:0005524; F:ArP binding; IEA.
GO:0019374; F:Bhotin binding; IEA.
GO:0016974; F:ligase activity; IEA.
GO:0016975; P:metabolism; IEA.
growth in Ustilago maydis.";
Mol. Gen. Cenet. 249:131-201(1995).
EMBL; 246886; CAA86983.1; -; Genomic_DNA
PIR; S60200; S60200.
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CPSASE 2; UNKNOWN 1
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BIOTINYL LIPOYL; 1
COA CT CTER; 1.
COA CT NTER; 1.
                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR005482; Biotin_carb_C
Interpro; IPR000089; Biotin_lipoyl
Interpro; IPR000022; Carboxyl_tran.
Interpro; IPR011763; COA_CT_C
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PF00289; CPSase_L_chain; 1.
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InterPro; IPRO11764; BC.
InterPro; IPRO01882; Biotin_BS.
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InterPro; IPR011762; COA_CT_N
InterPro; IPR005481; CPase_L N
InterPro; IPR005479; CPSase_D2_
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557; Conservative
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PS50975; ATP_G
PS50979; BC; 1
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PS50968; E
PS50989; C
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PS00866; CPSASE 1; 1. PS00867; CPSASE 2; UNKNOWN 1.
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                                                                                        429; Conservative
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                          Complete proteome. SEQUENCE 2237 AA;
                                                               Query Match
Best Local Similarity
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  PROSITE;
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DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL 540
             DSQFGHIPAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL
                                                                                                                                                                                                                               Cryptococcus neoformans var. neoformans JEC21.
Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,
Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                               Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D., Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E., Bosta M.R., Chibu R., Doering T.L., Donlin M.J., Bosdet I.E., Brent M.R., Grinberg V., Fu J., Fukushima M., Haas B.J. Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I., Kwon-Chung K.J., Lengeler K.B., Mairla R., Marra M.A., Marra R.E., Mathewson C.A., Mitchell T. Shumit R., Mickes B.L., Specht C.A., Shu B.B., Teinbey A., Shin H., Shumway M., Specht C.A., Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., Fraser C.M., Hyman R.W., The genome of the basidiomycetous yeast and human pathogen
                                                                                                                                                                                                                                                                                                                      Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback
Van Aken S., Fraser C.;
                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Acetyl-CoA carboxylase, putative.
ORFNames=CNF02180;
                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                          PRT; 2237 AA
                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=15653466; DOI=10.1126/science.1103773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; AE017346; AAW44009.1; -; Genomic_DNA QSKFC9; 24-557.
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InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR001032; Carboxyl_trans.
InterPro; IPR011762; COA_CT_C.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR005481; CPASSE_D.
InterPro; IPR005479; CPASSE_D.
Pfam; PP02185; Biotin_carb_C; I.
Pfam; PP02184; Biotin_lipoyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:biotin binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR011761; ATP GRASP.
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PS50968; BIOTINYL LIPOYL; 1
PS50989; COA_CT_CTER; 1.
PS50980; COA_CT_NTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01039; Carboxyl trans; 1.
Pfam; PF00289; CPSase L chain; 1.
Pfam; PF02786; CPSase L D2; 1.
PROSITE; PS50975; ATP GRASP; 1.
PROSITE; PS50979; BC; 1.
                                                                    DGLIQDRLTAERPPADLAV 560
                                                   DGLIQDRLTAERPPADLAV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cryptococcus neoformans.";
Science 307:1321-1324(2005).
                                                                                                                                         QEKFC9_CRYNE PRELIMINARY;
QSKFC9;
                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                      NCBI_TaxID=214684;
                                                                                                                                                                                                                                                                                                              STRAIN=JEC21;
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                                                                                                                                                                                                                                                                                        GTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQ 483
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                                                                                                                                                              63
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                                                                                                                                                                                      139 AVWAGWGHASENPRLPETLA--KSKIIFIGPPGSAMRSLGDKISSTIVAQHAKVPCMPWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 QKIIBEAPVIIAKPETPEEMEKAAVRLAKLVGYVSAGTVEYLYSHSDDSFYFLELNPRLQ
                                                                                                                                                                                                                                                             64 TFGDERALEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 TNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 EDGEKFKNSFQAVAGEVPGSPIFIMKTAGSARHLEVQLIADQYGNAISLFGRDCSVQRRH
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                                                                                                                                                        DHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYE
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Bukaryota; Pungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima Wickes B.L., Fu J., Davils R.W.,
Wickes B.L., Fu J., Davils R.W.,
"Cryptococcus neoformans serotype D sequencing.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                       5;
                                                   Length 2237;
                                                                                                       Indels
2237 AA; 248385 MW; E5BFB525BD89138E CRC64;
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Last annotation update)
                                                   78.1%; Score 2269; DB 2; 77.2%; Pred. No. 1.2e-145;
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                                                                                                    51; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572
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0550T6;
13-SEP-2005 (TEMBLEE] 31, C:
13-SEP-2005 (TEMBLEE] 31, L:
13-SEP-2005 (TEMBLEE], 31, L:
Hypothetical protein.
ORFNames=CNBF2550;
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65 FGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 FGNERAIQFTVMATPEDLAANADYIRMADQYVEVPGGTNNNNYANVELIVDVAERMDVHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 HKAVSOFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99087906; PubMed=9871120; DOI=10.1007/8002940050410;
Morrice J., MacKenzie D.A., Parr A.J., Archer D.B.;
"Isolation and characterisation of the acetyl-CoA carboxylase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                    Emericella nidulans (Aspergillus nidulans).
Bukaryota, Pungi, Ascomycota, Pezizomycotina, Burotiomycetes,
Burotiales, Trichocomaceae, Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0003999; F:acetyl-CoA carboxylase activity; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000374; F:biotin binding; IEA.
GO; GO:000815; P:metabolism; IEA.
GO; GO:000815; P:metabolism; IEA.
InterPro; IPR01761; ATP_GRASP.
InterPro; IPR01862; Biotin_BS.
InterPro; IPR001882; Biotin_Carb_C.
InterPro; IPR00089; Biotin_Lanb.
InterPro; IPR00089; Biotin_Lanb.
InterPro; IPR00022; Carboxyl_trans.
InterPro; IPR00022; Carboxyl_trans.
InterPro; IPR01763; COA_CT_N.
InterPro; IPR01763; COA_CT_N.
InterPro; IPR01763; COA_CT_N.
InterPro; IPR01763; COA_CT_N.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005481; CPase_LN.
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                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.3%; Score 2190; DB 2; 74.8%; Pred. No. 3.1e-140; iive 53; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Curr. Genet. 34:379-385(1998).
EMBL; Y1596; CAA75926.1; -; Genomic_DNA.
TYST, T30568; T30568.
HSSP, Q00955; LOD4.
SWR; O60033; 21-558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CPSASE 1; UNKNOWN 1
CPSASE 2; UNKNOWN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOTIN; 1.
BIOTINYL_LIPOYL; 1
                                                                                                                                                                                                         07, Created)
07, Last sec
                                                                                                                                                                                                                                                                                        Acetyl-CoA carboxylase (EC 6.4.1.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF01039; Carboxyl trans; 1.
PF00289; CPSase L chain; 1.
PF02786; CPSase L D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02785; Biotin carb \overline{C}; Pfam; PF00364; Biotin_lipoyl;
  | : :|:||| :||
| SS7 IAEGMISERPDPVVAV
                                                                                                                             O60033 EMENI PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from Aspergillus nidulans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 74.8
les 415; Conservative
                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS50975, ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FGSC A26
                                                                                                                                                                                                                                                                                                                   Name=accA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S:
Matches 415
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Pfam;
                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVWAGWGHASENPRLPETLA--KSKIIFIGPPGSAMRSLGDKISSTIVAQHAKVPCMPWS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 EDGEKFKNSFQAVAGEVPGSPIFIMKLAGSARHLEVQLIADQYGNAISLFGRDCSVQRRH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFGDERAIEFTVWATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVWAGWGHASENPRLPESLAASKHKIIPIGPPGSAMRSLGDKISSTIVAQHADVPCMPWS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQ 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQ 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 TNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKPOPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQ 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248325 MW; A99AF395A7CA2E8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.1%; Score 2269; DB 2; ilarity 77.2%; Pred. No. 1.2e-145; Conservative 51; Mismatches 74;
EMBL; AAEY01000031; EAL20176.1; -; Genomic_DNA.
                                                                                                                                                                                         InterPro; IFRO1682; Biocin BS.
InterPro; IPRO1682; Biocin BS.
InterPro; IPRO1682; Biocin Carb C.
InterPro; IPRO10029; Biocin Lipoyl.
InterPro; IPRO10029; Carboxyl trans.
InterPro; IPRO11762; COA CT C.
InterPro; IPRO11762; COA CT C.
InterPro; IPRO5401; CPSase D2 ATP bd.
Pfam; PPO1039; CPSase D2 ATP bd.
Pfam; PPO1039; Carboxyl trans; 1.
Pfam; PPO1039; Carboxyl trans; 1.
Pfam; PPO1039; Carboxyl trans; 1.
Pfam; PPO1039; Carboxyl trans; 1.
Pfam; PPO1039; Carboxyl trans; 1.
PROSITE; PS50975; ATP GRASP; 1.
PROSITE; PS509975; BC; I.
PROSITE; PS50980; COA CT CTER; 1.
PROSITE; PS50980; COA CT TRER; 1.
PROSITE; PS50980; COA CT TRER; 1.
PROSITE; PS500866; CPSASE 1; UNKNOWN 1.
PROSITE; PS500866; CPSASE 1; UNKNOWN 1.
                                        GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:biotin binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
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                                                                                   RPQPKGHTTACRITSEDPGEGFKPSSGTWHELNFRSSSNVWGYFSVGTAGGIHSFSDSQF
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Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
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GEBO04;

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10-MAY-2005 (TEMBLE1 30, L6

10-MAY-2005 (TEMBLE1 30, L6

Hypothetical protein.
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                                                                                                                                                                   InterPro; IPR001882; Biotin BS.
InterPro; IPR001882; Biotin carb C.
InterPro; IPR000089; Biotin carb C.
InterPro; IPR000089; Biotin lipoyl.
InterPro; IPR001022; Carboxyl trans.
InterPro; IPR011763; COA CT N.
InterPro; IPR011762; COA CT N.
InterPro; IPR005481; CPaSeE LN.
InterPro; IPR005481; CPaSeE LN.
Pfam; PF00285; Biotin carb C; I.
Pfam; PF00289; Carboxyl trans; I.
Pfam; PF00289; Carboxyl trans; I.
Pfam; PF00289; Carboxyl trans; I.
Pfam; PF00289; CPSSSE L. Chain; I.
PROSITE; PS50975; ATP-GRASP; I.
PROSITE; PS50979; BC; I.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:biotin binding; IEA.
GO; GO:0016874; F:biogase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR011761; ATP GRASP.
InterPro; IPR011764; BC.
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320 KIIEEAPVTIAKPATFQAMERAAVSLGKLVGYVSAGTVEYLYSHADDKFYFLELNPRLQV 379
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EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                              GHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLI
                                                                                                                                                                                                                                                                                                                                    Bukaryota, Fungi, Ascomycota; Pezizomycotina, Sordariomycetes;
Sordariomycetidae, Sordariales; Sordariaceae; Neurospora.
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Last annotation update)
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; AABX01000166; EAA33781.1; -; Genomic_DNA
; P24182; 1DV1.
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GC:000374; F.biotin binding; IEA.
GC:0016874; F.ligase activity; IEA.
GC:0008152; P:metabolism; IEA.
eIPro; IPR011761; AIP_GRASP.
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Hypothetical protein.
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A Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
Bowyer M., Fedorova N., Fedorova N., Feldblyum T.V., Davies R., Oyer P.S.,
Roldman G.H., Gond K., Garcia J.L., Garcia M.J., Goble A.,
Goldman G.H., Gond K., Griffith-Jones S., Gwilliam R., Haas B.,
Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
Kumagai T., Lafton A., Large J.P., Li W., Lord A., Lu C.,
Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
Rabbinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
Renauld H., Robson G.D., Rodriguez de Cordobe S., Rodriguez-Pena J.M.,
Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIIBEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEPAFLELNPRLQV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 FGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 NGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQ 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 HNLPSHFIGGNHLDAAPPSSVKDFVASHEGHSVISSVLIANNGIAAVKEIRSVRKWAYET 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S., Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J., White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K., Machida M., Hall N., Barrell B., Denning D.W.; Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 HKAVSQFIGGNPLETAPASPVADPIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYET
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                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Pungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=330879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                PRT;
                                                                                                                                                                                                            Created)
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13-SEP-2005 (TrEMBLrel. 31, Le
13-SEP-2005 (TrEMBLrel. 31, Le
Acetyl-CoA carboxylase.
ORFNames-Atu2008670;
Aspergillus fumigatus Af293.
559 SNKLTAERPDTTIAV 573
                                                                                                                 2_ASPFU
Q4XIV2_ASPFU PRELIMINARY;
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Best Local Similarity 74.2
Matches 412; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A£293;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                     139 VWAGWGHASENPKLPESLAASPKKIVFIGPPGSAMRSLGDKISSTIVAQHADVPCIPWSG 198
                                                                                                                                                                                                                                                                                                                 TGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCT 244
                                                                                                                                                                                                                                                                                                                              NGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQ 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPOPOGHVVACRITAENPDIGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQF 484
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                                                                                                                                                                                                                                 FGDERA I EFTVMATPEDLKVNADY I RMADQYVEVPGGSNNNNYANVDL I VDVAERAGVHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYET
                                                                                                                                                                    Gaps
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
NCBI_TaxID=242507;
                                                                                                                                               Length 2275;
                                                                                                                                            Query Match 75.0%; Score 2179; DB 2; Length 2 Best Local Similarity 74.1%; Pred. No. 1.7e-139; Matches 411; Conservative 57; Mismatches 87; Indels
                                                                                                                          254563 MW; B6A8B175C023D5BD CRC64;
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Last annotation update)
Pfam, PF01039; Carboxyl_trans; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00786; CPSase_L_chain; 1.
PROSITE; PS50975; ATP_GRASP; 1.
PROSITE; PS50979; BC; 1.
PROSITE; PS50969; BIOTIN; 1.
PROSITE; PS50989; COA_CT_TER; 1.
PROSITE; PS50980; COA_CT_TER; 1.
PROSITE; PS50980; COA_CT_TER; 1.
PROSITE; PS50980; COA_CT_MIER; 1.
PROSITE; PS00866; CPSASE_1; UNKNOWN 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN 1.
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13-SEP-2005 (TrEMBLrel. 31,
Hypothetical protein.
ORFNames-MG07613.4;
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QSIYC2;
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                                                                                                                         2275 AA;
                                                                                                                 Hypothetical
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                                                                                                                         SEQUENCE
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Best Local
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RA Altren B., Nusbaum C., Abben A., Abouellall A., Adekoya E., Aderson M., Anderson S., Att-zahra M., Allen N., Allen T., Abouellall A., Adekoya E., Archchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A., Bayul T., Blitehbereyn B., Bloom T., Blye J., Cangor K., Chang J., Changarata J., Campor K., Chang J., Changarata J., Campor K., Chang J., Cheshatesang Y., Citroen M., Rollymore A., Considine T., Cook A., Cooke P., Corum B., Coulon C., R. Dorie K., Dorrie L., Duffer S., Dodge S., Dooley K., Dorrie P., R. Brickson J., Farina A., Faro S., Perreira P., Flicher H., Hafer N., All J., Ramoer T., Barna D., Ganado D., Garandoois E., Gyalteen K., Hafer N., Andrew A., Honde W., Haudey D., Garandoois E., Gyalteen K., Hafer N., Andrew A., Honde W., Hadden J., Ramponian D., Hagos B., Hall J., Hatcher B., Haller A., Higgins H., Rama D., Landers E., Katu A., Kamar M., Houde W., Hughes L., Hulme W., Hagins H., Lama D., Landers T., Legar J., Lewis D., Lewis T., Labutti K., Lama D., Landers T., Legar J., Lokyitsang Y., Lucien O., Luichlad-ton K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O., Mandlad. J., Marabella R., Maru K., Matchews C., Mauceli E., Moru K., Matchews C., Mauceli E., Moru K., Matches T., Machan T., Moru K., Matches C., Nayen C., Mauce J., Moru K., Mandlad J., Morus L., Munson G., Naylor J., Naves C., Nguyen C., Nowes J., Milalev A., Milacan D., Phulkhang P., Fiqani B., Norbu N., O'domenl P., Decary S., Omotosho B., Parker S., Perrin D., Phulkhang P., Fiqani B., Retta R., Richardson S., Rise C., Route C., Stude C., Settipalli S., Sharpe T., Sharpe T., Rohner J., Rohner D., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharpe T., Sharp
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EMBL, AZU01000922; EAA53336.1; -; Genomic_DNA.

Hypothetical protein.

SEQUENCE 2344 AA; 262098 MW; E2FE164E451733D6 CRC64;
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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258 ATEEEGFEALYKAAASEIPGSPIFIMKTAGNARHLEVQLLADQYGNNISLFGRDCSVQRR
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                                                                                                                                                                                                                                                                         18 PYFNIADHFIGGNRLANAPSGKVKDFVAQNDGHTVITNVLIANNGIAAVKEIRSVRKWAY
                                                                                                                                                                                                                                                                                                                               63 ETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGV
                                                                                                                                                                                                                                                                                                                                                      18 ETFRDERAIHFTVMATPEDLQANAEYIRMADHYVEVPGGTNNHNYANVELIVDIAERMNV
                                                                                                                                                                                                                                                                                                                                                                                                                              HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 CTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498 QFGHIFAYGENRSASRKHMYMALKELSIRGDFRTTIEYLIKLLETEAFEDNTISTGWLDE
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|Q00955 Saccharomyces cerevisiae YNR016c ACC1 acetyl-CoA
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STRAIN=CBS 2359 / IFO 1267 / NREL Y-1140 / WM37;
PubMed=15229592; DOI=10.1038/nature02579;
Dujon B., Sherman D., Fieder G., Durrene P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Gofffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
                                                                                                                                                                               Gaps
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                                                                                                                              Length 2271;
                            Indels
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                               90;
                                                                                                                              Score 2148; DB 2;
Pred. No. 2.3e-137;
preliminary data.
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                                                                                                                                                                            64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                              73.9%;
llarity 72.4%;
Conservative 6
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LISKRLTAERPETMLAV
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QCCL34;
                                                                                                                                                       Similarity
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Best Local S:
Matches 403
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Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
Buckgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
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                                                                                                                                                                                                                                                                                424
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          VWAGWGHASENPKLPESLAASPKKIIFIGPPGSAMRSLGDKISSTIVAQHAQVPCIPWSG 217
                                                                                                                                                       NGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQ 304
                                                                                                                                                                                                                                                       KIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364
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Bukaryota; Mungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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Submitted (FBE-2004) to the BMBL/Genbank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which
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Last annotation update)
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Q41878;
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ORFNames=FG06580.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=PH-1;
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567

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388 EHPTTEMVTGVNLPSAQLQIAMGIPMHRIRDIRLLYGVDPKSASEIDFNFSTPESAKTQR 447
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X. PubMed=1522952; DOI=10.1038/nature02579;

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A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

A Barnay S., Blanchins S., Beckerich J.-M., Beyne E., Bleykasten C.,

B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

B Boisrame A., Boyer E., Fairhead C., Ferry-Dumazet H., Groppi A.,

A Rerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

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Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

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Mincker P., Souciet J.-L.;

Mincker P., Souciet J.-L.;

Mincker P., Souciet J.-L.;

Mintre 430:35-44 (2004)
                                                                                   KPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQF
                                                                                                                             KPTPKGHCTACRITSEDPNEGFKPSGGALHELNFRSSSNVWGYFSVGNNGGIHSFSDSQF
                                                                                                                                                                                                                       GHIFAYGADRSEARKQMVISLKELSIRGDFRITTVEYLIKLLETDAFESNKITTGWLDGLI
                                                                                                                                                                                                                                                             508 GHIFAFGENRQASRKHMVVALKELSIRGDFRTTVEYLIKLLETEDFEDNTITTGWLDDLI
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome L complete sequence.
OrderedLocusNames=CAGLOL107899;
Candida glabrata (Yeast) (Torulopsis glabrata)
Eukaryota, Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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SMR; QGFKK8; 15-566, 1482-2218.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000374; F:Ligase activity; IEA.

GO; GO:000374; F:Ligase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR011761; ATP_GRASP.

InterPro; IPR01182; Biotin_BS.

InterPro; IPR00182; Biotin_lipoyl.

InterPro; IPR00089; Biotin_lipoyl.

InterPro; IPR00089; Biotin_lipoyl.

InterPro; IPR011763; COA_CT_C.

InterPro; IPR011763; COA_CT_C.

InterPro; IPR011763; COA_CT_C.

InterPro; IPR011763; COA_CT_C.

InterPro; IPR011763; COA_CT_C.

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InterPro; IPR011764; IPR011764; COA_CT_C.

InterPro; IPR011764; IPR011764; COA_CT_C.

InterPro; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764; IPR011764;
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PROSITE; PSS0979; BC; 1.
PROSITE; PS00188; BIOTIN; 1.
PROSITE; PSS0968; BIOTINYL_LIPOYL; 1.
                                                                                                                                                                                                                                                                                                                                                           545 QDRLTAERPPADLAV 559
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QEFKK8;
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28 KLASHFIGLNIYUDKADDSPLKEFVKSHGCHTVISKVLIANNGIAAVKEIRSVRKWAYETF 87
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PS50968; BIOTINYL LIPOYL; 1.
PS50969; COA_CT_CTER; 1.
PS50980; COA_CT_NTER; 1.
PS00866; CPSASE_1; UNCNOWN 1.
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Matches 392; Conservative
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P78820; 09457; 009447; 009576; 009616; 009667;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Acetyl-CoA-carboxylase (EC 6, 4.1.2) (ACC) (Cell untimely torn protein 6) [Includes: Biotin carboxylase (EC 6.3.4.14)].
Name=cut6; ORFNames=SPAC56E4.04c; Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                               IFAYGADRSEARKOWVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQD
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                                                                                                                                                                                            Length 2233;
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                                                                                                                                2233 AA; 250049 MW; 8B381EA1F3C99FC3 CRC64;
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Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                         DB 2;
                                                                                                                                                                                   71.9%; Score 2090.5; DB 2; 70.7%; Pred. No. 1.9e-133; ive 73; Mismatches 86;
                   PS50980; COA_CT_NTER; 1.
PS00866; CPSASE_1; UNKNOWN 1.
PS00867; CPSASE_2; UNKNOWN 1.
PS50989; COA_CT_CTER; 1
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KMTAKKPDPILAV 581
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NCBI_TaxID=4896;
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RI SUBLIGIOR 1986 (1986) to the EMEL/GenBank/DDED databases.

RE MICLEGYIDS SEQUENCE (LARGE SCALE GROWIC DNA).

REPLIKES-21884014 pubMedialises9560, DOE-10 1038/ARLINE 754.

REPLIKES-21884014 pubMedialises9560, DOE-10 1038/ARLINE 754.

REPLIKES-21884014 pubMedialises9560, DOE-10 1038/ARLINE 1024.

REPLIKES-21884014 pubMedialises9560, DOE-10 1038/ARLINE 1024.

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REPLIKES-21884014 pubMedialises9560, DOE-10 1038/ARLINE 1024.

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REPLIKES-21884014 pubMedialises950, DOE-10 1038/ARLINE 1024.

REPLIKES-21884014 pubMedialises950, DOE-10 1038/ARLINE 1024.

REPLIKES-21884014 pubMedialises960, DOE-10 1038/ARLINE 1024.

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REPLIKES-21884014 pubMedialises960, DOE-10 1038/ARLINE 1024.

REPLIKESTIVE CONTAIRS 10 1039/ARLINE 1024.

REPLIKESTIVE CONTAIRS 10 1039/ARLINE 1024.

REPLIKESTIVE CONTAIRS 10 1039/ARLINE 1024.
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STEKFAQAFQOVLDELPGSPVFVMKLAGQARHLEVQILADQYGNNISLFGRDCSVQRRHQ 336
                                                                                                                                                                                                   97 NNERAIKFTVMATPDDLKVNADYIRMADQYVEVPGGSNNNNYANVELIVDIAERMNVHAV 156
                                                                                                                                  245 NGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQ 304
                                                                                                                                                                                   KIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A fafontaine I., de Montigny J., Marck C., Neuvegliee C., Talla E.,
A fafe M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Bospons L., Rabre E., Fairhead C., Ferry-Dumazer H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Swennen D., Tekaia F., Richard G. F., Straub M.-L., Suleau A.,
A Swennen D., Tekaia F., Mesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
A Wincker P., Souciet J.-L.,
                                         157 WAGWGHASENPKLPEMLSASSKKIVFIGPPGSAWRSLGDKISSTIVAQSARVPCMSWSGN
                           WAGWGHASENPRLPESLAASKHKIIPIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGT
                                                                              186 GIKETMMSDQ-GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCT
                                                                                            EHPTTEMVSGVNI PAAQLQVAMGI PLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQR
                                                                                                                                                                                                                                                                                              KPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQF
                                                                                                                                                                                                                                                                                                                                                GHIFAYGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carboxylase.
OrderedLocusNames=YALIOC11407g;
OrderedLocusNames=YALIOC11407g;
Yarrowia lipolytica (Candida lipolytica).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|Q00955 Saccharomyces cerevisiae Acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
STRAIN=CLIB 122 / E 150;
PubMed=15229592; DOI=10.1038/nature02579;
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EMBL; CR382129; CAG82031.1; -; Genomic_DNA.
SMR; OCCC91, 33-574.
SMR; OCO05524; F:ATP binding; IEA.
GO; GO:0009374; F:biotin binding; IEA.
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Q6CC91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                       Biotin, Complete proteome, Fatty acid biosynthesis, synthesis, Multifunctional enzyme, Nucleotide-binding,
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                                                                                                                                                                                                                                                                                                                                                                                                               ATP (By similarity).
By similarity.
By similarity.
Biotin (covalent) (By similarity).
Coenzyme A (By similarity).
Coenzyme A (By similarity).
Coenzyme A (By similarity).
LYAIKATISLPRLFYRRLRTMAPRVASHF -> RF
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TIN (in Ref.
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ive 62; Mismatches 96; Indels
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                                                                                                                                                                                                                                                                                                                                                               Biotin carboxylation.
                                                                                                                                                                                                                                                                                                                                                                           ATP-grasp.
Biotinyl/lipoyl.
Carboxyltransferase.
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(in Ref. 1
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LMKSEPST -> SN
K -> N (in Ref
R -> H (in Ref
F -> L (in Ref
V -> Y (in Ref
                                                                                        InterPro; IPR011763; COA_CT_C.
InterPro; IPR011762; COA_CT_C.
InterPro; IPR005491; CPASE_L.
InterPro; IPR005491; CPASE_L.
Pfam; PF02785; Biotin carb_C; I.
Pfam; PF00346; Biotin lipoyl; I.
Pfam; PP01039; Carboxyl trans; I.
Pfam; PP01039; CPSASE_L.Chanh; I.
Pfam; PP01099; CPSASE_L.Chanh; I.
Pfam; PF02786; CPSASE_L.Chanh; I.
PROSITE; PS0975; ATP_GRASP; I.
PROSITE; PS0979; BC; I.
  division; IMP
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                                                   Biotin_carb C.
Biotin_lipoyl.
Carboxyl trans.
COA CT C.
                                                                                                                                                                                                                                                      LIPOYL;
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             InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
                                      Biotin_BS
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Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                     Ligase, Lipid synthesis;
                                                 Interpro; IPR005482; BInterpro; IPR00089; BInterpro; IPR000020; CInterpro; IPR011763; CInterpro; IPR011763; C
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                                        InterPro; IPR001882;
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PROSITE,
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BINDING
BINDING
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BINDING
CONFLICT
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131 HASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKET 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 FIGLNTVEQAEASPLRDYVRLHGGHTVISKILIANNGIAAVKEIRSVRKWAYETFGDGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 IEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 HASENPLLPEKLARSKRKVVFIGPPGSAMRSLGDKISSTIVAQHAKVPCIPWSGTGVDQV
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                                                                                                                                                                                                                                                                                                                                          PubMed=15001715; DOI=10.1126/science.1095781;
PubMed=15001715; DOI=10.1126/science.1095781;
PubMed=15001715; DOI=10.1126/science.1095781;
PubMed=15001715; DOI=10.1126/science.1095781;
Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavier A., Gaffney T.D., Philippsen P.;
The Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome.";
Science 304:304-307(2004).
EMBL, AE016814; AAS50436.1; -; Genomic_DNA.
                                                                                                                                                                                                                                  Saccharomycetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2231 AA; 249717 MW; 5024EA7C7873B842 CRC64;
                                                                                                                                                                                                      Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota, Pungi, Ascomycota, Saccharomycotina, Sacc
Saccharomycetales, Saccharomycetaceae, Eremothecium
                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.2%; Score 2069.5; DB 2 70.4%; Pred. No. 5.2e-132;
                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                      2231 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ); IPR000022; CCA CT C.
); IPR011762; CCA CT C.
); IPR011762; CCA CT C.
); IPR01641; CPASE L N.
); IPR005479; CPSSSE D2 ATP bd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0005524; F:ATP binding; IEA.
GO:0009374; F:bictin binding; IEA
GO:0016874; F:ligase activity; IEA
GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00866; CPSASE_1; UNKNOWN_1
PS00867; CPSASE_2; UNKNOWN_1
                                                      PRT;
                                                                                                Created)
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PP00364; Biotin_lipoyl; 1.
PP01039; Carboxyl_trans; 1.
PP00289; CPSase_L_chain; 1.
PP02786; CPSase_L_D2; 1.
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PS50989; COA CT CTER;
PS50980; COA CT NTER;
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InterPro; IPR011764; BC.
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PS50979; BC: 1.
                                                                                           05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                      Q75EK8_ASHGO PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 70.49
Matches 387; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00022; C
InterPro; IPR011763; C
InterPro; IPR011762; C
InterPro; IPR005481; C
                                                                                                                                                                                                                                                                            NCBI_TaxID=33169;
                                                                                                                                                              AAR071Wp.
Name=AAR071W;
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                                 SEK8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKTQRKPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEY 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PWSGTGIKETMM-SDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 IRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2266 AA; 251115 MW; 8B581AF5F9374E4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.7%; Score 2084; DB 2; 71.2%; Pred. No. 5.4e-133; ive 63; Mismatches 96;
                                                                                       InterPro; IPR001882; Biotin_BS.
InterPro; IPR001882; Biotin_BS.
InterPro; IPR001842; Biotin_Carb C.
InterPro; IPR001022; Carboxyl_trans.
InterPro; IPR001022; Carboxyl_trans.
InterPro; IPR001763; COA_CT_C.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005491; CPase_D2_ATP_bd.
Pfam; PF00184; Biotin_Carb_C?, IPR00548; Biotin_Carb_C?, IPR00548; Biotin_Lipoyl; I.
Pfam; PF00189; Craboxyl_trans; I.
Pfam; PF00189; Craboxyl_trans; I.
Pfam; PF00189; CPSase_L_D2; I.
PR005TIE; PS50979; ATP_GRASP; I.
    F:ligase activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                 B; BIOTIN; UNKNOWN 1.

B; BIOTINYL LIPOYL; 1.

9; COA_CT_CTER; 1.

0; COA_CT_NTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00866; CPSASE 1; UNKNOWN 1
PS00867; CPSASE 2; UNKNOWN 1
                              P:metabolism; IEA 761; ATP_GRASP.
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LDELISNKLTAERPDSFLAV 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.24
Matches 399; Conservative
GO, GO:0016874; F:liga
GO, GO:0008152; P:meta
InterPro, IPR011761; A
InterPro, IPR011764; B
                                                                                                                                                                                                                                                                                                                                                                                                              PS50979; BC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           120968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 WCHASENPLLPEKLAASPKKIIFIGPPGSAMRSLGDKISSTIVAQHAQVPCIPWSGTGVD 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 TTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQ 427
                                                                                                                                                                                                                                                                                                                                             ETMMSDQ-GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 NFITLYNQAANEIPGSPIFIMKLAGDARHLEVQLLADQYGTNISLFGRDCSVQRRHQKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490 PKGHCTACRITSEDPGEGFKPSGGSLHELNFRSSSNVWGYFSVGNQSSIHSFSDSQFGHI
                                                                                                                                                                                                                                                                                                                          9 SQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 EFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 PQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHI
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                                                                                                                                                                                                                                                             DB 2; Length 2271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-0C7-1996 (Rel. 34, Last Bequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Includes: Biotin
                                                                                                                                                                                                                                 253422 MW; D57D403C36D7A290 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carboxylase (EC 6.3.4.14)].
Name=FAS3; Synonyms=ACC1; OrderedLocusNames=YNR016C;
                                                                                                                                                                                                                                                             70.9%; Score 2061.5; DB 2 70.7%; Pred. No. 1.9e-131; ive 63; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2233 AA
           Pfam; PF00285; Biotin_carb C; I.
Pfam; PF00364; Biotin_lipol; I.
Pfam; PF001039; Carboxyl_trans; I.
Pfam; PF001039; Carboxyl_trans; I.
Pfam; PF00289; CPSase_Lchain; I.
Pfam; PF002786; CPSase_Lchain; I.
PROSITE; PS50979; BC; I.
PROSITE; PS50979; BC; I.
PROSITE; PS50989; COA_CT_TER; I.
PROSITE; PS50980; COA_CT_TER; I.
PROSITE; PS50980; COA_CT_TER; I.
PROSITE; PS50980; COA_CT_TER; I.
PROSITE; PS50986; COA_CT_TER; I.
PROSITE; PS50986; CPSASE_I; I.
PROSITE; PS50986; CPSASE_I; I.
PROSITE; PS50986; CPSASE_I; I.
PROSITE; PS50986; CPSASE_I; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast)
D2_ATP_bd.
                                                                                                                                                                                                                                                                             Best Local Similarity 70.78
Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      548 LTAERPPADLAV 559
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                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 2271 AA; ;
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LTAERPDPIVAV
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Q00955;
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COAC_YEAST
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                                                              APVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTT 369
                                                                                                                                                                    EMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQ 429
                                                                                                                                                                                    GHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFA 489
                                                                                                                                                                                                                                                                                          490 YGADRSEARKOMVISLKELSIRGDFRITVEYLIKLLETDAFESNKITTGWLDGLIQDRLT 549
                                                                                                                                                                                                                                                                                                            Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O., Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W., Jones T., Scherer S., Agabian N.; "Amnotation of the Genome of Candida albicans "; Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AACQ01000039; EAK99708.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=SC5314;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
Davis R.W., Scherer S.;
"The diploid genome sequence of Candida albicans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           liploid genome sequence of Candida albicans."; Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:Biotin binding; IEA.
GO; GO:0008152; F:Bigses activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR011761; ATP GRASP.
InterPro; IPR011764; BC.
InterPro; IPR011882; Biotin BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biotin_carb_C.
Biotin_lipoyl.
Carboxyl_trans.
COA_CT_C.
COA_CT_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein ACC1.
Name=ACC1; OkFNames=CaO19.7466;
Candida albicans SC5314.
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                                                                                                                                                                                                                                                                                                                                                       AERPPADLAV 559
                                                                                                                                                                                                                                                                                                                                                                                       581
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InterPro; IPR005481;
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Philippsen P., Kleine K., Poellmann R., Duesterhoeft A., Hamberg K., Hegemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K., Altmann R., Altmann R., Altmann R., Altmann R., Altmann R., Altmann R., Altmann R., Altmann R., Altmann R., Altmann R., Altmann R., Beinhauer J.D., Boskovic J., Buitrago M.J., Bussereau F., Coster F., Crouzet M., D'Angelo M., Dall Pero F., De Antoni A., del Rey F., Doignon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M., Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N., Albert C., Garcia-Cantalejo J.M., Glansdorff N., Jimenez A., Jonnaux J.-L., Karfinger-Hartl L., Lanfranchi G., Lepingle A., Levesque H., Lyck R., Maftahi M., Mallet L., Maurer C.T.C., Nicaud J.-M., Nawes H.-W., Moestl D., Nasr F., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nicaud J.-M., Nica
                                                                                                        NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 2015-2022.
MEDLINE-92262474; PubMed=1350093;
Al-Feel W., Chirala S.S., Wakil S.J.;
"Cloning of the yeast FAS3 gene and primary structure of yeast acetyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carrier protein, biotin carboxylase, and carboxyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENZYME REGULATION: By phosphorylation.
PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION SITE SER-1157.

MEDILINE-21864552; PubMed=11875433; DOI=10.1038/nbt0302-301;

MEDILINE-21864552; PubMed=11875433; DOI=10.1038/nbt0302-301;

Pricatro S.B., McCleland M.L.; Stukenberg P.T., Burke D.J., Ross M.M., Shabanowitz J., Hunt D.F., White F.M.;

"Phosphoptroctoome analysis by mass spectrometry and its application to Saccharomyces cerevisiae."

Nat. Biotechnol. 20:301-305(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2) = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coenzyme A carboxylase.";
Science 299:2064-2067(2003).
-!- FUNCTION: This protein carries three functions: biotin carboxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTAKLOGRAPHY (2.7 ANGSTROMS) OF 1429-2233 IN COMPLEX WITH COA, MUTAGENESIS OF LEU-1705; ARG-1731; TYR-1738 AND ARG-1954, AND HOMODIMERIZATION.
  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=12663926; DOI=10.1126/science.1081366;
Zhang H., Yang Z., Shen Y., Tong L.;
"Crystal structure of the carboxyltransferase domain of acetyl-
                       Saccharomycetales, Saccharomycetaceae, Saccharomyces, NCBI TaxID=4932,
                                                                                                                                                                                                                      CoA carboxylase.";
Proc. Natl. Acad. Sci. U.S.A. 89:4534-4538(1992)
                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=97313269; PubMed=9169873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFACTOR: Biotin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + malonyl-CoA.
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PS00866; CF 1738 1731 1954 1994 PROSITE; PROSITE; PROSITE; PROSITE; DOMAIN NP BIND ACT\_SITE BINDING MOD RES MUTAGEN BINDING MUTAGEN MUTAGEN SINDING SINDING MUTAGEN MUTAGEN OMAIN DOMAIN This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed. SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Contains 1 ATP-grasp domain.
SIMILARITY: Contains 1 biotin carboxylation domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
SIMILARITY: Contains 1 carboxyltransferase domain.

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GO; GO:0005789; C:endoplasmic reticulum membrane; IDA.
GO; GO:0005739; C:mitochondrion; IDA.
GO; GO:0005989; F:acetyl-CoA carboxylase activity; IMP.
GO; GO:0004075; F:biotin carboxylase activity; IMP.
GO; GO:0006989; P:nuclear membrane organization and biogenesis; TAS.
GO; GO:0006606; P:protein-nucleus import; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-grasp.
Biotinyl/lipoyl.
Carboxyltraneferase.
ATP (By similarity).
By similarity.
Biotin (covalent) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphoserine.
L->1: Raises Km for malonyl-CoA by
factor of 20.
R->S: Raises Km for malonyl-CoA by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor of 15.
Y->F: No effect.
Y->F: No effect.
factor of 70.
E->O: Lowers activity 10-fold.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D-structure; ATP-binding; Biotin; Complete proteome;
Direct protein sequencing; Patty acid biosynthesis; Ligase;
Lipid synthesis; Multifunctional enzyme; Nucleotide-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W -> G (in Ref. 1).
I -> IWYRCL (in Ref. 1).
AINGML -> ESTWA (in Ref. 1).
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             M92156; AAA20073.1; -; Unassigned DNA Z71631; CAA96294.1; -; Genomic_DNA.
                                                                                                                                                                                                                          Ensembl; YNRO16C; Saccharomyces cerevisiae.
SGD; S000005299; ACC1.
                                                                                                                                                                                                                                                                                                                                                InterPro; PR001764; BC.
InterPro; PR001862; Biotin_BS.
InterPro; PR001862; Biotin_Carb C.
InterPro; PR0000842; Biotin_Carb C.
InterPro; PR000089; Biotin_lipoyl.
InterPro; PR000089; Biotin_lipoyl.
InterPro; PR000089; CAP C.
InterPro; PR001762; COA CT C.
InterPro; PR001763; COA CT C.
InterPro; PR001763; COA CT C.
InterPro; PR0017649; COA CT C.
InterPro; PR001849; COA CT C.
Pfam; PR0189; Biotin_lipoyl.;
Pfam; PR00189; Carboxyl_trans; 1.
Pfam; PR0189; CPSase L. Chain; 1.
Pfam; PR0189; CPSase L. Chain; 1.
PROSITE; PS50979; BC; 1.
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        EMBL, M92156; AAA20073.1; -; Unassig EMBL, 271631, CAA96294.1; -; Genomic PIR, 102147; S63347; S63347; S63347; S63347; S63347; S63347; S63347; SFB; 1002; X-ray; A/B=1429-2233. PDB; 1004; X-ray; A/B/C=1482-2218. PDB; 10VY; X-ray; A/B/C=1482-2218. PDB; 10VY; X-ray; A/B-C=1482-2218. PDB; 10VY; X-ray; A/B-C=1462-2218. PDB; 10VY; X-ray; A/B-C=1462-2218. PDB; 10VY; X-ray; A/B-C=1462-2218. PDB; 10VY; X-ray; A/B-C=1462-2218. PDB; 10VX; X-ray; A/B-C=1462-2218. PDB; 10VX; X-ray; A/B-C=1466. PDB; 10VX; X-ray; A/B-C=1466. PDB; 10VX; X-ray; A/B/C=1466.
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GermOnline; 143361;
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STRAIN-ATCC 36239 / CBS 767;
PubMed=15229592; DOI=10.1038/nature02579;
Bujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
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Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
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25-OCT-2004 (TYEMBLrel. 28, Last sequence update)
25-OCT-2004 (TYEMBLrel. 28, Last annotation update)
Similar to CA5816|CaACCl Candida albicans CaACCl acetyl-coenzyme-A
carboxylase.
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Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                     8;
                                                               Length 2233;
                                                                                                                  89; Indels
      0A335AAD9B1F8308 CRC64
                                                   70.9%; Score 2060; DB 1; 69.1%; Pred. No. 2.3e-131; iive 76; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2297
250353 MW;
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DDLITHKMTAEKPDPTLAV
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Q6BX58;
2233 AA;
                                                                                 Similarity
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SEQUENCE
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Nature 430:35-44 (2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 GDERAIQFTVWATPEDLEANAEYIRMADQPIEVPGGTNNNNYANVELIVEIAERTNVDAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 WAGWGHASENPLLPEMLAASPKKILFIGPPGSAMRSLGDKISSTIVAQHADVPCIPWSGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.2%; Score 2039.5; DB 2; 69.4%; Pred. No. 6.1e-130; ive 72; Mismatches 97;
                                                                                                                                                                                   EMBL; CR382134; CAG85206.1; -; Genomic_DNA.
SMR; Q6BX58; 79-628, 1547-2257.
GQ; GG:0005524; F:ATP binding; IEA.
GQ; GG:000374; F:biotin binding; IEA.
GQ; GG:0016874; F:ligase activity; IEA.
GQ; GG:0008152; F:metabolism; IEA.
IILEPPO; IRPR011/61, ATP GRASP.
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR011764; BC.
InterPro; IPR011764; BC.
InterPro; IPR001882; Biotin Carb C.
InterPro; IPR000089; Biotin Tarb C.
InterPro; IPR000029; Biotin Tipoyl.
InterPro; IPR001763; CoA CT C.
InterPro; IPR011763; COA CT C.
InterPro; IPR011763; COA CT N.
InterPro; IPR01841; CPaRe I N.
InterPro; IPR005481; CPARe I N.
Fram; PP02765; Biotin Carb C; I.
Pfam; PP00264; Biotin Carb C; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
PROSITE; PS50975; ATP_GRASP; 1.
PROSITE; PS50979; BC; 1.
PROSITE; PS50979; BC; 1.
PROSITE; PS50989; COA_CT_CTER; 1.
PROSITE; PS50989; COA_CT_CTER; 1.
PROSITE; PS50980; COA_CT_CTER; 1.
PROSITE; PS50866; CPSASE_1; UNKNOWN 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF01039; Carboxyl trans; 1.
PF00289; CPSase L chain; 1.
PF02786; CPSase L D2; 1.
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InterPro,
InterPro,
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                     628
                                                                                                                                                                                                                                                                                                                                                                                                                                     HFA1 protein.

Name=HFA1; OrderedLocusNames=YMR207C; ORFNames=YM8261.01C, YM8325.08C;
Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Identification of a Saccharomyces cerevisiae gene closely related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAS3 (acetyl-CoA carboxylame).";
DNA Seq. 4:69-70(1993).
-!- COFACTOR: Biotinn (By similarity).
-!- SIMILARITY: Contains 1 ATP-grasp domain.
-!- SIMILARITY: Contains 1 biotin carboxylation domain.
-!- SIMILARITY: Contains 1 biotinyl-binding domain.
-!- SIMILARITY: Contains 1 biotinyl-binding domain.
-!- SIMILARITY: Contains 1 biotinyl-binding domain.
-!- SIMILARITY: Contains 1 carboxyltransferase domain.
-!- CAUTION: The reading frame from which this protein in translated has no Met initiation codon near to the 5'end. It does not seem the a pseudogene. There are no apparent frameshifts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97313268 | AB972; MEDLINE=97313268 | PubMed=9169872; MEDLINE=97313268 | PubMed=9169872; MEDLINE=97313268 | PubMed=9169872; MEDLINE=97313268 | PubMed=9169872; Medles S., Chirlingworth T., Connor R., Deviln K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A. Rice P., Skelton J., Walsh S.V., Whitchead S., Barrell B.G., The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII."
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EWRL; Z2558; CAA88647.1; -; Genomic_DNA.
EWRL; Z25589; S55089.
FIRSP; G00955; 1004.
SMR; P32874; 90-634.
EMBL; Z2589; S55089.
HXSP; G00955; 1004.
SMR; P32874; 90-634.
Ensembl; YMR207C; Saccharomyces cerevisiae.
SGD; S00004920; HFA1.
GG, GO:0005399; F:acetyl-CoA carboxylase activity; IGI.
GO; GO:0006539; P:facty acid biosynthesis; IGI.
InterPro; IPR011764; BC.
InterPro; IPR011764; BC.
InterPro; IPR011764; BC.
InterPro; IPR011764; BC.
InterPro; IPR011764; BC.
                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                       2273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 125-949.
MEDLINE=94146412; PubMed=7906156;
Kearsey S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biotin BS
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629 SKKLTSERPDHIVAV 643
                                                                                                                                                              545 QDRLTAERPPADLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
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P32874;
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62 YETFGDERALEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 VHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 WSGTGIKETMMSDQ--GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 IRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORRHOKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIQUEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDAVWAGWGHASENPCLPELLASSORKILFIGPPGRAMRSLGDKISSTIVAQSAKIPCIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKTORKPOPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480 ADSOPGHIFAYGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDSQFGHIFAVGNDRQDAKQNMVLALKDFSIRGEFKTPIEYLIELLETRDFESNNISTGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      proteome, Ligase, Nucleotide-binding. Biotin carboxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-grasp.
Biotinyl/lipoyl.
Carboxltransferase.
ATP (By similarity).
By similarity.
Biotin (covalent) (By similarity).
F -> L (in Ref. 2).
F -> L (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 2273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 1.1e-119; 86; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.0%; Score 1889.5;
                                                                                                                    ATP bd
Biotin_lipoyl.
Biotin_lipoyl.
Carboxyl_trans.
                                                     InterPro; IPR011763; COA CT C.
InterPro; IPR011763; COA CT C.
InterPro; IPR001762; COA CT N.
InterPro; IPR005481; CP866 D. N.
InterPro; IPR00549; CP8066 D. APP Pfam; PP00286; Biotin carb C; I.
Pfam; PP00364; Biotin carb C; I.
Pfam; PP00364; Biotin lipoyl; 1.
Pfam; PP00389; CP806, Interps; 1.
Pfam; PP00289; CP806 L. Chain; I.
PROSITE; PS50979; ATP GRASP; I.
PROSITE; PS50979; BC; I.
PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                  BIOTINYL LIPOYL;
COA CT CTER; 1.
COA CT NTER; 1.
CPSASE 1; 1.
CPSASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.38;
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Best Local Similarity 64.3%;
Matches 355; Conservative
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ATP-binding; Bioti
JOMAIN 134
                                                                                                                                                                                                                                                                                                       PS50968;
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332
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360 PRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPES 419
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                           IRKCTNGEBFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSV
                                                                                                                                                                                                    420 PKTORKPOPOGHVVACRITAENPDTGPKPGMGALTELNFRSSTSTWGYFSVGTSGALHEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Sinilhikova O.W., Ginolhac S.M., Magnard C., Leone M., Anczukow O., Moreau K., Thompson D., Coutanson C., Bonadona V., Lasset C., Goldgar D.E., Joulin V., Dalla Venezia N., Lenoir G.W.;
Goldgar D.E., Joulin V., Dalla Venezia N., Lenoir G.W.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; A7237919; AAE69841.1; -; mRNA.

EMBL; A7237919; AAE69841.1; -; mRNA.

EMBL; A73731919; AAE69841.1; -; mRNA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR011761; ATP GRASP.

R InterPro; IPR011861; BC.

R InterPro; IPR005482; Biotin Garb C.

InterPro; IPR005482; Biotin Carb C.

InterPro; IPR00022; Caboxyl trans.

InterPro; IPR01763; COA CT C.

InterPro; IPR01763; COA CT C.

InterPro; IPR01763; COA CT C.

InterPro; IPR005491; CFSase D2 ATP bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Acetyl-CoA carboxylase alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00188; BIOTIN; 1.
PS50968; BIOTINYL_LIPOYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF02785; Biotin carb C; T.
PF00364; Biotin_lipoyl; 1.
PF01039; Carboxyl_trans; 1
PF00289; CPSase L_chain; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02786; CPSase_L_D2; 1. PROSITE; PS50975; ATP_GRASP; 1 PROSITE; PS50979; BC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fam; PF02785; Biotin_carb_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEXDA8 HUMAN PRELIMINARY;
QEXDA8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDGLIQDRLTAE 551
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Q6XDA8_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSGTGIKETMMSDQ--GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 2273;
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                                                                                                                                                                                                                                       Acetyl-coenzyme A carboxylase like carboxylase (Fragment) Name=ALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saito A., Kazuta Y., Kondo H., Tanabe T.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; D78165; BAA24410.1; -; Genomic_DNA.
HSSP; Q00955; 10D4.
SWR; O42823; 90-634.
                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259162 MW; BF6C01982FCB5DEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ennembl. YMR207C; Saccharomyces cerevisiae. GO; GO:0005524; F:ATP binding; IEA. GO; GO:0005524; F:ATP binding; IEA. GO; GO:000514; F:Ligase activity; IEA. GO; GO:0016874; F:Ligase activity; IEA. GO; GO:0016874; F:Ligase activity; IEA. InterPro; IPR011764; BC. InterPro; IPR011764; BC. InterPro; IPR011862; Biotin_BS. InterPro; IPR001892; Biotin_lipoyl. InterPro; IPR000099; Biotin_lipoyl. InterPro; IPR000099; Biotin_lipoyl. InterPro; IPR001763; COA_CT_C. InterPro; IPR01763;  CPase_E.N. InterPro; IPR005491; Cphp synth_L.D. Pfam; PF001054; Biotin_lipoyl; I. Pfam; PF001054; Biotin_lipoyl; I. Pfam; PF001054; GPSase_L. Chall; I. Pfam; PF001059; CPSase_L. L. Pfam; PF001059; CPSase_L. L. Pfam; Pf001059; CPSase_L. L. Pf001059; CPSase_L. L. Pf001059; CPSase_L. L. Pf001059; CPSase_L. L. Pf001059; CPSase_L. L. Pf001059; CPSase_L. L. L. Pf001059; CPSase_L
                                                                                                                      2273 AA
                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
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2; UNKNOWN 1
                                                                                                                   PRT;
                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50980; COA_CT_NTER; 1
PROSITE; PS00866; CPSASE_1; UNKN
PROSITE; PS00867; CPSASE_2; UNKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSS0975; ATP GRASP; 1.
PSS0979; BC; 1.
LDDLILKNLSSD 641
                                                                                                            042823_YEAST PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 64.3
Matches 355; Conservative
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2273 AA;
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PROSITE;
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SEQUENCE
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=22709197; PubMed=12810950; DOI=10.1073/pnas.1332670100;
Mao J., Chirala S.S., Wakil S.J.;
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                                                                                                                      Length 2346;
                                                                                                                                                         Indels
PS50989; COA_CT_CTER; 1.
PS50980; COA_CT_NTER; 1.
PS00866; CPSASE_1; 1.
PS008667; CPSASE_2; UNKNOWN 1.
2346 AA; 265554 MW; F1F0AS18F8824FFC CRC64;
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Last annotation update)
                                                                                                                  61.6%; Score 1791; DB 2; I
63.8%; Pred. No. 6e-113;
ive 79; Mismatches 103;
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Matches 345; Conservative
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63.6%; Pred. No. 1.1e-112;
live 79; Mismatches 104; Indels
                                       HSSP; P24182; IDV1.
Ensembl; ENSG0000132142; Homo sapiens.
Ensembl; ENSG0000132142; Homo sapiens.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008174; F:bictin binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0018152; P:metabolism; IEA.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
InterPro; IPR001882; Biotin_BS.
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InterPro, IPR000089, Biotin_lipoyl.
InterPro, IPR000022, Carboxyl_trans.
AAP94122.1; -; mRNA
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NUCLEOTIDE RESULT 23 셤

PHOSPHORYLATION SITE SER-1200.
MEDLINE=90337981; PubMed=1974251;
Kong I.-S., Lopez-Casillas F., Kim K.-H.,;
"Acetyl-CoA carboxylase mRNA species with or without inhibitory coding sequence for Ser-1200 phosphorylation.",
J. Biol. Chem. 265:13695-13701(1990). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Rattus. P11497; P97902; 01-OCT-1989 (Rel. 12, Created) 01-OCT-1989 (Rel. 12, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin Name-Acaca; Synonyms-Acac; STRAIN=Wister; TISSUE=Liver;
MEDLINE=94237850; PubMed=7910165;
Winz R., Hess D., Aebersold R., Brownsey R.W.;
"Unique structural features and differential phosphorylation of the 280-kDa component (isozyme) of rat liver acetyl-CoA carboxylase.";
J. Blol. Chem. 269:14418-14445(1994).
-: FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis "Structure of the coding sequence and primary amino acid sequence of Luo X.N., Park K., Lopez-Casillas F., Kim K.-H.; Structural features of the acetyl-CoA carboxylase gene: mechanisms for the generation of mRNAs with 5' end heterogeneity."; Proc. Natl. Acad. Sci. U.S.A. 86:4042-4046(1989). MEDLINE=89289706; PubMed=2567668; Bai D.-H., Moon T.-W., Lopez-Casillas F., Andrews P.C., Kim K.-H.; "Analysis of the biotin-binding site on acetyl-CoA carboxylase from MEDLINE=88296498; PubMed=2900138; Munday M.R., Campbell D.G., Carling D., Hardie D.G.; Identification by amino acid sequencing of three major regulatory phosphorylation sites on rat acetyl-CoA carboxylase."; Eur. J. Biochem. 175:331-338 (1988). MEDLINE=89214151; PubMed=2565337;
Lopez-Casillas F., Kim K.-H.;
"Heterogeneity at the 5' end of rat acetyl-coenzyme A carboxylase mRNA. Lipogenic conditions enhance synthesis of a unique mRNA in liver."; NUCLEOTIDE SEQUENCE (ISOFORM 1).
MEDLINE=88320328; PubMed=2901088;
Lopez-Casillas F., Bai D.-H., Luo X., Kong I.-S., Hermodson M.A.,
Kim K.-H.; PROTEIN SEQUENCE OF 76-85 AND 1198-1201, AND PHOSPHORYLATION NUCLEOTIDE SEQUENCE OF 1167-1200 (ISOFORMS 1 AND 2), AND acetyl-coenzyme A carboxylase."; Proc. Natl. Acad. Sci. U.S.A. 85:5784-5788(1988) PARTIAL PROTEIN SEQUENCE, AND MASS SPECTROMETRY. 2345 AA Eur. J. Biochem. 182:239-245(1989) Biol. Chem. 264:7176-7184(1989) NUCLEOTIDE SEQUENCE (ISOFORM 1). MEDLINE=89264558; PubMed=2566999; NUCLEOTIDE SEQUENCE OF 1-33 STANDARD; Rattus norvegicus (Rat) BIOTIN-BINDING SITE. 632 V 632

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not of long-chain fatty acids. This protein carries three functions: biotin carboxyl carrier protein, biotin carboxylase, and carboxyltransferase.

CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate + malonyl-CoA.

CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2) = ADP + phosphate + carboxyblotin-carboxyl-carrier protein. -!- COFACTOR: Biotin. -!- ENZYME REGULATION: By phosphorylation. -!- PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting) -!- PTM: The N-terminus is blocked.
-!- SIMILARITY: Contains 1 ATP-grasp domain.
-!- SIMILARITY: Contains 1 biotin carboxylation domain.
-!- SIMILARITY: Contains 1 biotinyl-binding domain.
-!- SIMILARITY: Contains 1 carboxyltransferase domain. Event=Alternative splicing; Named isoforms=2; sold=P11497-2; Sequence=VSP\_011753; IsoId=P11497-1; Sequence=Displayed; step.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS; Name=1; Name=2 +

DNA -; NOT\_ANNOTATED\_CDS; mRNA. EMBL; J03808; AAA40653.1; -; mRNA. EMBL; M26731; AAA40652.1; -; Genomic EMBL; M26195; AAA40654.1; -; mRNA. ; AAA40654.1; -; max.; AAA40655.1; -; mRNA.; AAA40655.1; -; mRNA. M26196; AAA40655.1; M26197; AAA40656.1; removed. EMBL;

Ensembl; ENSRNOG00000034013; Rattus norvegicus ATP bd Biotin\_carb\_C.
Biotin\_lipoyl.
Carboxyl\_trans. Pfam; PF00289; CRIDOXY1 trans; 1.
Pfam; PF00289; CPSase L Chain; 1.
PROSITE; PS50975; ATF GRASP; 1.
PROSITE; PS50979; BC; 1.
PROSITE; PS00188; BIOTIN; 1 fam; PF02785; Biotin carb C; 1 fam; PF00364; Biotin lipoyl; 1 fam; PF01039; Carboxyl trans; InterPro; IPR011763; COA\_CT\_C.
InterPro; IPR011762; COA\_CT\_N.
InterPro; IPR005481; CPaae\_I\_N.
InterPro; IPR005479; CPSaee\_D2. InterPro; IPR011761; ATP\_GRASP. Biotin BS. InterPro; IPR001882; InterPro; IPR005482; InterPro; IPR000089; EMBL; M55315; -; NOT PIR; A35578; A35578. HSSP; Q00955; 10D4. InterPro; IPR011764; InterPro; IPR000022; 621248; Acac RGD;

BIOTINYL LIPOYL; 1. COA CT CTER; 1. COA CT NTER; 1. COSASE 1; 1. CPSASE 2; 1. PROSITE; PS50980; PS00866; PROSITE; PS50989; ROSITE, PS50968

Alternative splicing; ATP-binding; Biotin; Direct protein sequencing; Fatty acid biosynthesis; Ligase; Lipid synthesis; Multifunctional enzyme; Nucleotide-binding; Phosphorylation.

116 617 Biotin carboxylation. ATP-grasp PS00867; PROSITE; 1

Carboxyltransferase ATP (Potential) By similarity. Biotin (covalent). Biotinyl/lipoyl. NP BIND ACT SITE BINDING **DOMAIN** 

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LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QG-F 197
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 to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                           61.4%; Score 1783.5; DB 2; 63.8%; Pred. No. 2.1e-112; ive 73; Mismatches 108;
            EMBL; AY451394; AAS13686.1; -; mRNA.
GO; GO:0009343; C:biotin carboxylase complex;
GO; GO:0005524; F:ArP binding; IEA.
GO; GO:0004075; F:biotin carboxylase activity;
GO; GO:0006874; F:ligase activity; IEA.
GO; GO:000152; P:metabolism; IEA.
InterPro; IPRO11761; ATP GRASP.
                                                                                                                                                                                                       InterPro; IRRO02114; HPT SerP 5.

Pfam; PR002185; Biotin carb C; 1.

Pfam; PR00284; Biotin carb C; 1.

Pfam; PR00289; Carboxyl trans; 1.

Pfam; PR00289; CPSase_L_chain; 1.

Pfam; PR02286; CPSase_L_chain; 1.

PR0SITE; PS50975; ATP GRASP; 1.

PR0SITE; PS50975; ATP GRASP; 1.

PR0SITE; PS50999; COA CT CTER; 1.

PR0SITE; PS50989; COA CT CTER; 1.

PR0SITE; PS00866; CPSASE 1; UNKNOWN 1.

PROSITE; PS00867; CPSASE 2; UNKNOWN 1.

PROSITE; PS00867; CPSASE 2; UNKNOWN 1.

PROSITE; PS00867; CPSASE 2; UNKNOWN 1.

PROSITE; PS00867; CPSASE 2; UNKNOWN 1.
                                                                                                Interpro; IPR011764; BC.
Interpro; IPR005482; Biotin_carb_C.
Interpro; IPR000089; Biotin_lipoyl.
Interpro; IPR010022; Carboxyl trans.
Interpro; IPR011763; COA_CT_C.
Interpro; IPR011763; COA_CT_N.
Interpro; IPR005481; CPase_L.N.
Interpro; IPR005481; CPase_L.N.
Interpro; IPR005419; Cphp_synth_L.D2.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                            Gaps
                                                                                                                                                           14;
                                                                                                                                  Length 2345;
Coenzyme A (By similarity).
Coenzyme A (By similarity).
Coenzyme A (By similarity).
Phosphoserine.
Phosphoserine.
                                                                                                                                                           Indels
                                                                             Missing (in isoform 2).
/FTId=VSP 011753.
W; 78E9CF9ADE1E8771 CRC64;
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Last annotation update)
                                                                                                                                61.4%; Score 1785; DB 1;
llarity 63.6%; Pred. No. 1.5e-112;
Conservative 80; Mismatches 103;
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ID GGJIZO MOUSE PRELIMINARY;
DC GGJIZO,
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DT 05-JUL-2004 (TrEMBLrel. 27, La
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DF 05-JUL-2004 (TrEMBLrel. 27, La
GN Name=Acacb;
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NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Heart;
Mao J., Wakil S.J.;
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NCBI_TaxID=10090;
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Matches 344; Conserv
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199 TVSDDVYQQACIHTABEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKOLYNAVLG 258
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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PubMed=15302935; DOI=10.1073/pnas.0404720101;
PubMed=15302935; DOI=10.1073/pnas.0404720101;
Beausoleil S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,
Li J., Cohn M.A., Canteley L.C., Gygi S.P.;
"Large-scale characterization of HeLa cell nuclear phosphoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 101:12130-12138/2004).
-! FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis of long-chain fatty acids. This protein carries three functions: biotin carboxyl carrier protein, biotin carboxylase, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           013085;
01-NOV-1997 (Rel. 35, Created)
10-NOV-1997 (Rel. 35, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin carboxylase (EC 6.3.4.14)].
Name=ACACA; Synonyme=ACAC, ACCI, ACCA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver;
MEDLINE-95249602; PubMed=7732023;
Abu-Elheiga L., Jayakumar A., Baldini A., Chirala S.S., Wakil S.J.;
Ahu-Elheiga L., Jayakumar A., Baldini A., Chirala S.S., Wakil S.J.;
"Human acetyl-CoA carboxylase: characterization, molecular cloning, and evidence for two isoforms.";

    + malonyl-CoA.
    -! - CATALYIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
    -! - COFACTOR: Biotin.
    -! - ENZYME REGULATION: By phosphorylation (By similarity).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 92:4011-4015(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carboxyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    559 V 559
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  142
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COA1 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 ASP-AEFVTRFGGNKVIEKVLIANNGIAAVKCMRSIRRWSYEMFRNERAIRFVVMVTPED
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ASPVADFIRKOGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.3%; Score 1783; DB 2; Length 2 63.6%; Pred. No. 2.1e-112; ive 79; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50968; BIOTINYL LIPOYL; 1.
PS50989; COA CT CTER; 1.
PS50980; COA CT NTER; 1.
PS00866; CPSASE 1; UNKNOWN 1.
PS00867; CPSASE 2; UNKNOWN 1.
2345 AA; 265Z55 MW; 6995C534B054FE02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.

Li, ML596447; CAI25271.1; -; Genomic_DNA.

Li, AL59625; CAI24019.1; -; Genomic_DNA.

Li, AL59625; CAI25271.1; JOINED; Genomic_DNA.

Li, AL596447; CAI24019.1; JOINED; Genomic_DNA.

GO:0009343; C:blotin carboxylase complex; IEA.

GO:000554; F:ATP binding; IEA.

GO:000554; F:ATP binding; IEA.

GO:000554; F:blotin binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                      01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                 PRT; 2345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0004075; F:biotin carboxylase act.,
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016812; P:metabolism; IEA.
InterPro; IPR01176; ATP_GRASP.
InterPro; IPR01176; BC.
InterPro; IPR01176; BC.
InterPro; IPR00189; Biotin_Garb.
InterPro; IPR00089; Biotin_Garb.
InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR001176; COA_CT.
InterPro; IPR01176; COA_CT.
InterPro; IPR01176; COA_CT.
InterPro; IPR01176; COA_CT.
InterPro; IPR05481; CPase_L N.
InterPro; IPR05481; CPase_L N.
InterPro; IPR05481; CPase_L N.
InterPro; IPR05481; CPase_L N.
InterPro; IPR05481; Cphp_synth_L_D2.
INTERPRO; IPR065481; Cphp_synth_L_D2.
INTERPRO; IPR065481; Cphp_synth_L_D2.
INTERPRO; IPR065481; INTERPRO; IPR065481; INTERPRO; IPR065481; INTERPRO; IPR065481; INTERPRO; IPR065481; INTERPRO; IPR065481; INTERPRO; IPR065481; INTERPRO; INTERPRO; IPR065481; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; INTERPRO; 
                                                                                                                                                                                                                                          Acetyl-Coenzyme A carboxylase.
Name=Acac; ORFNames=RP23-123010.1-001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Carboxyl_trans; 1.; CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02786; CPSase LD2; 1.
PROSITE; PS50975; ATP GRASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; BIOTIN; 1.
                                                                                                                          OSSWU9 MOUSE PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344; Conservative
                                                                                                                                                                                                                                                                                                                                                      Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fracey A.;
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PROSITE; 1
PROSITE; 1
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PROSITE; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
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                764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; A
EMBL; A
EMBL; A
                                                                                                                                                   05SW09
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ઠ 셤 ઠે g 280 NVPQELYEKGYVKDVDDGLKAAEKVGYPVMIKASEGGGGKGIRKVNNADDFPNLFRQVQA 339

EVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPED

199 TVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLG 258

LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QGFL 198

LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141

82

142 222

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthesis;
   PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.3%; Score 1781; DB 1; Length 2346;
63.6%; Pred. No. 2.9e-112;
ive 79; Mismatches 104; Indels 14; Gaps
                          UNGELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: Expressed in brain, placental, skeletal muscle, renal, pancreatic and adipose tissues; expressed at level in pulmonary tissue; not detected in the liver. SIMILARITY: Contains 1 ATP-grasp domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (covalent) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67, CPSASE_2; 1.
iotin; Fatty acid biosynthesis; Ligase; Lipid
1 enzyme; Nucleotide-binding; Phosphorylation.
7 618 Biotin carboxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphoserine (By similarity)
Phosphoserine (By similarity)
Phosphoserine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9519190D40190D14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coenzyme A (By similarity)
Coenzyme A (By similarity)
Coenzyme A (By similarity)
                                                                                                                                                                                                                                                                                                                                                            30; GO:0003989; F:acetyl-CoA carboxylase activity; TAS.
InterPro; IRR011761; ATP_GRASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carboxyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biotinyl/lipoyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphoserine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity
Biotin (covale
                                                                                                                                                                                                                                                                                           HSSP; Q00955; 10D4.
Ensembl; ENSG00000132142; Homo sapiens.
HGNC; HGNC:84; ACACA.
MIM; 200350; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000022; Carboxyl trans.
InterPro; IPR011763; COA_CT_C.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR00181; CPase_L N.
InterPro; IPR005479; CPSase_D2_ATP_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                            carb C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00188; BIOTIN; 1. PS00188; BIOTINYL LIPOYL; PS50986; COA CT CTER; 1. PS50980; COA CT NTER; 1. PS00866; CPSĀSE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005482; Biotin_BS.
InterPro; IPR005089; Biotin_carb_InterPro; IPR000089; Biotin_lipoy_InterPro; IPR000022; Carboxyl_trailnterPro; IPR011763; COA_CT C.
                                                                                                                                                                                                                                                                EMBL; U19822; AAC50139.1; -; mRNA.
PIR; I38928; I38928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan, PF02785; Biotin carb C; 1.
Pfam, PF00364; Biotin_lipoyl; 1.
Pfam, PF01039; Carboxyl_trans; 1.
Pfam, PF00289; CRSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265040 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50975, ATP GRASP, 1
PS50979; BC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02786; CPSase L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Bi
                                                                                                                                                                                                                                                                                                                                                                                               interPro;
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MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
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499 KQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLA 558

559 V 559

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AENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498 SENPDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFAGSQFGHCFSWGENREEAI 571

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MEDLINE=20196006 PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Geroge R.A., Lewis S.E., Richards S.A. Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R.; Miklos G.L.G., Abbril J.F., Abbayani A., An H.-J., Andrews-Pfannkoch C., Baddwin D., Ballew R.M., Basu A., Barman B.P., Bhardari D., Botchiar P., Brotchiar P., Brotchiar P., Brotchiar P., Brotchiar P., Borkova D., Botchan M.R., Bouk B., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dietz S.M., Dodson K., Doup D.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Ibegwam C.,
                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                     01-MXY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
110-MAY-2005 (TrEMBLrel. 30, Last annotation update)
CG11198-Pb. isoform B (GH12002p).
ORFNames-CG11198;
                                                                                                                              2323 AA
                                                                                                                       Q9V346_DROME PRELIMINARY, Q9V346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
     632 V 632
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ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED

Best Local Similarity 63.6 Matches 344; Conservative

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                 Ketchum K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halpern A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22426069; PubMed=12537572; Misthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminher J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=2242665; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A. Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pedifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter (Weinstock G., Scherer S.E., Wyers B.W., Glbbs R.A., Rubin G.M.; melanogaster euchromatic genome shotgun: release 3 of the Drosophila Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Svirskas R.,
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Celniker S., Carlson J., Wan K., Pfeiffer B., Frise
Hoskins R., Stapleton M., Pacleb J., Park S., Svirsk
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Biol. 3: RESEARCH0084.1-RESEARCH0084.20(2002)
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VMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKA 326
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PROSITE; PS50989; COA_CT_CTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS00866; CPSASE 1; UNKNOWN 1.
PROSITE; PS00867; CPSASE 2; UNKNOWN 1.
SEQUENCE 2323 AA; 261921 MW; 4F27D73A05CEB645 CRC64;
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        the EMBL/GenBank/DDBJ databases
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Submitted (JUN-2002) to the EMBL/GenBank/DD
EMBL; AE003839; AAF59156.2; -; Genomic_DNA.
EMBL; AY119502; AAM50156.1; -; mRNA.
                                                                                   HSSP; Q00955; 10D4.
FlyBase; PBGn0033246; CG11198.
G) GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:biocin binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
                                                                                                                                                                                                                                                                                                                 InterPro; IPR001882; Biotin BS.
InterPro; IPR001882; Biotin carb C.
InterPro; IPR001089; Biotin lipoyl.
InterPro; IPR0010193; Carboxyl trans.
InterPro; IPR011763; COA CT C.
InterPro; IPR011762; COA CT N.
InterPro; IPR001549; CPASE D. A.
InterPro; IPR005481; CPASE D. A.
Pfam; PF002785; Biotin carb C; I.
Pfam; PF00364; Biotin lipoyl; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01039; Carboxyl_trans; 1.
Pfam; PF00289; CPSase L_chain; 1.
Pfam; PF02786; CPSase L_D2; 1.
PROSITE; PS50975; ATP_GRASP; 1.
PROSITE; PS50979; BC; 1.
PROSITE; PS00188; BIOTIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carboxyltransferase.
CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver,
MEDLINE=87106011; PubMed=2879745; DOI=10.1016/0014-5793(87)81564-8;
Takai T., Wada K., Tanabe T.;
"Primary structure of the biotin-binding site of chicken liver acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENZYME REGULATION: By phosphorylation.
PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)

    + malonyl-CoA.
    CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
    = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
    COFACTOR! Blotin.

                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 212:98-102(1987).
-!- FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis of long-chain fatty acids. This protein carries three functions: biotin carboxyl carrier protein, biotin carboxylase, and
                                                                                                                                                                                                                                                                             Takai T., Yokoyama C., Wada K., Tanabe T.;
"Primary structure of chicken liver acetyl-CoA carboxylase deduced
BLSIRGDFRTTVEYLITLETNRFLDNSIDTAWLDALIAERVQSEKPDILLGV
                                                                                 01-07L-1989 (Rel. 11, Created)
01-07L-1989 (Rel. 11, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Acetyl-CoA carboylase (EC 6.4.1.2) (ACC) [Includes: Biotin carboxylase (EC 6.3.4.14)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 ATP-grasp domain.
SIMILARITY: Contains 1 biotin carboxylation domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
SIMILARITY: Contains 1 carboxyltransferase domain.
                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
                                                              Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, Q00955; 10D4.
Ensembl; ENSGALGO0000005439; Gallus gallus.
InterPro; IPR011761; ATP_GRASP.
                                                              2324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Call.

; COA_CT_C.

;; COA_CT_N.

1; CPABE_L N.

1; CPABE_L D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biotin_carb_C.
Biotin_lipoyl.
Carboxyl_trans.
COA_CT_C.
                                                                                                                                                                                                                                                                                                    from cDNA sequence.";
J. Biol. Chem. 263:2651-2657(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J03541; AAA48701.1; -; mRNA.
EMBL; X05019; CAA28675.1; -; mRNA.
                                                                                                                                                                                                                                                               MEDLINE=88139305; PubMed=2893793;
                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 493-820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biotin_BS
                                                              STANDARD;
                                                                                                                                                              Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR011764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR011763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR005479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A29924; A29924.
                                                                                                                                                                                                                                                                                                                                                                                                          CoA carboxylase.";
                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                  TISSUE=Liver
                                                            CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                removed.
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438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L--HKNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWNGSGLRVDWQENDLQKRIL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 EVPGSPIFVMRLAKQSRHLEVQILADQYGNAISLFGRDCSVQRRHQKIIEEAPASIATSV 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AENPDIGFKPGMGALTELNFRSSISTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 LAASKHKIIPIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETWMSD---QGFL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400 VFEHWEQCAVKLAKAVGYVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPCTEMVADVNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKANAEYIKWADHYVPVPQGPININNYANVELILDIAKRIPVQAVWAGWGHASENPKLPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAOLOVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMVVALKELSIRGDFRITVEYLIKLLETESFQQNRIDTGWLDRLIAEKVQAERPDTMLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SENPDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFADSQFGHCFSWGENREEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2324;
                                                                                                                                                                                             PROSITE; PS50969; BIOTINYL LIPOYL; 1.
PROSITE; PS50969; COA_CT_CTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS00866; CP5ASE_1; 1.
ATP-binding; Biotin; Direct protein sequencing;
Patry acid biosynthesis; Ligase; Lipid synthesis;
Multifunctional enzyme; Nucleotide-binding; Phosphorylation.
DOMAIN 117 618
Biotin carboxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphoserine (By similarity)
Phosphoserine (By similarity)
Phosphoserine (By similarity)
WM, 3FICS41F01BBBEFG CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 1780; DB 1; Length 2; Pred. No. 3.4e-112; 81; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coenzyme A (By similarity)
Coenzyme A (By similarity)
Coenzyme A (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biotinyl/lipoyl.
Carboxyltransferase.
ATP (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
Biotin (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.2%; Score 1780;
Pfam; PF00364; Biotin_lipoyl; 1. Pfam; PF00164; Biotin_lipoyl; 1. Pfam; PF00289; Carboxyl_trans; 1. Pfam; PF00289; CPSase_L_D2; 1. PROSITE; PS50975; ATP_GRASP; 1. PROSITE; PS50979; BC; 1.
                                                                                                                                                                                     PROSITE, PS00188; BIOTIN, 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.4%
Matches 343; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1193 11
2324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1800
2104
2106
78
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                                                                                                                                                                                                                                                                                         RAMEDLINE-20196005, PubMed-10731132; DOI=10.1126/Science.287.5461.2185; RAMEDLINE-20196005, PubMed-10731132; DOI=10.1126/Science.287.5461.2185; RAMEDLINE-20196005, PubMed-10731132; DOI=10.1126/Science.287.5461.2185; RAMEDLINE-20196005, RAMED S.E., Lib W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Lib W., Hoskins R.A., Galle R.F., Surden G.R., Mortman J.R., Yandell M.D., Zhang Q., Champe M., Pfeiffer B.D., RAMED R. C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., RAMED R. C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., RAMED R. C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., RAMED R. C., Rogers Y.-H.C., Blazel R.G., Mortman G., Borker B.G., Bellew R.M., Basu A., Baxendale J. J., Andrews-Ffannkoch C., Bladwin D., Ballew R.M., Basu A., Baxendale J. B., Bardari D., Bolahako V., RAMETI J.F., Agbayani A., Burler H., Cadleu E., Center A., Chandra I., R. Benge P.V., Bernam B.P., Bardari D., Bolahako V., Burkis K.C., Busam D.A., Bullke C. Davangor K.J. Cantel R. B., Churt A., Candriel R., Downes M., Dugan-Rochis S., Durkov B.C., Dunn P., Durbin K.J., Evaley S., Dahlke C. Davangor K.J., Evaley R.A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., Gabriel I., R., Goldre C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Jerraz C., Jerraz R., Houck J., Mei M.-H., Ibegwam C., Jalai M., Kalush P., Rapen G.H., Ke Z., Kannison J.A., Kechum K.A., Jalai M., Kalush F., Kalver C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liasko P., Lei Y., Leviteky A.A., Li J.H., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Leviteky A.A., Li J.H., Muzny D.M., Nalson D.L., Nather C. McLeod M.P., Muzny D.M., Nather E., Mortman G.S., Pan S., Pollard J., Muzny D.M., Nather E., Spradling A.C., Stapleton M., Strong R., Smith T., Stue R., Roder K.A., Nixon K., Naussern D., Puri, Wang Z.-Y., Wassarman D.A., Weiner E., Wang Z.-Y., Wassarman D.A., Weiner E., Shang K.H., Wang Z.-Y., Wassarman D.A., Weiner E., Shang X.H., Wang Z.-Y., Wassarman D.A., Weiner E., Shang X.H., Roder C., Stapleton M., Strong R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleron M., Sutton G.G., Venter C., Weinstrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                              01-MAY_2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAX_2004 (TrEMBLrel. 26, Last sequence update)
01-MAX_2004 (TrEMBLrel. 26, Last annotation update)
CG11198-PA, isoform A.
Name=CG11198. ORFNames=CG11198;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCB1_TaxID=7227;
                                                                            PRT; 2482 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINE=22426070; PubMed=12537573;
                                                                         O9V347_DROME PRELIMINARY;
                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
 632 V 632
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DROME
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87 DYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASK 146
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Pride E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE-22426069; PubMed=12537572;
MEDLINE-22426069; PubMed=12537572;
Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P. Bettendourt B.R., Celniker S.E., de Grey A.D.N.J., Drygdale R.A., Bettendourt B.R., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2482;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278596 MW; FOB6D2B15C676A4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003839; AAF59155.2; -; Genomic_DNA.
HSSP; Q00955; 10D4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                 Genome Biol. 3: RESEARCH0084.1-RESEARCH0084.20 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Biol. 3: RESEARCH0083.1-RESEARCH0083.22 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 3.7e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.2%; Score 1780; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000042, InterPro; IPR011763, COA_C1_C. InterPro; IPR011762, COA_CT_N. InterPro; IPR005481, CPage_LN. InterPro; IPR005479; CPage_LN. IPR005479; CPage_D2_ATP_bd. IPR005479; CPage_D2_ATP_bd. IPR005479; CPage_D2_ATP_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0031246; CG11198.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:biotin binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPSASE 1; UNKNOWN 1.
CPSASE 2; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR001882; Biotin BS.
PR005482; Biotin carb C.
PR000089; Biotin lipoyl.
PR000022; Carboxyl trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF01039; Carboxyl trans; 1.
PF00289; CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOTINYL LIPOY
COA CT CTER; 1
COA CT NTER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50975; ATP_GRASP; 1.
PROSITE; PS50979; BC; 1.
PROSITE; PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 342; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001882;
InterPro; IPR005482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [5]
NUCLEOTIDE SEQUENCE
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PS00867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50968;
PROSITE; PS50989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50980;
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COA1 BOVIN
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PROSITE; 1
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SEQUENCE
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EYIKMADHYVPVPGGSNNNNYANVELIVDIALRTQVQAVWAGWGHASENPKLPELL--HK 366
                                                         ::|:||| || :|||||::|:|||| |::| :|||| ::| :||||::| EGLVFLGPPERAMWALGDKVASSIVAQTAEIPTLPWSGSDLKAQYSGKK--IKISSELFA 424
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                                                                                                                                                                                                                  HKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQ
                                                                                                                QACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVF
                                                                                                                                      AVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNI PAAQLQVAM
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELSIRGDFRITVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AY451393; AAS13685.1; -; mRNA.
MGI; MGI:108451; Acaca.
GG; GO:0003989; Facetyl-CoA carboxylase activity; IMP.
InterPro; IPR011761; ATP GRASP.
InterPro; IPR011764; BC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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InterPro; IPR001022; Carboxyl trans.
InterPro; IPR011763; CoA CT C.
InterPro; IPR011763; COA CT C.
InterPro; IPR011763; COA CT C.
InterPro; IPR005481; CPSSE I.N.
InterPro; IPR00549; CPSSE I.N.
Pfam; PP002785; Biotin_carb_C; I.P.
Pfam; PP001099; Carboxyl trans; I.P.
Pfam; PP001099; CRSSE L. Chain; I.P.
Pfam; PP001099; CPSSE L. Chain; I.P.
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InterPro; IPR000089; Biotin_lipoyl.
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PS50975; ATP GRASP; 1.
PS50979; BC; 1.
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STRAIN=C57BL/6J; TISSUE=Liver;
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Mus musculus (Mouse).
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PS50968; 1
PS50989;
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PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                             LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
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MEDLINE-21378179; PubMed=11485560; DOI=10.1042/0264-6021:3580127;
MED. Marcos S., Davis S.K., Burzlaff J., Seyfert H.-M.;
"Genomic distribution of three promoters of the bovine gene encoding acetyl-COA carboxylase alpha and evidence that the nutritionally regulated promoter I contains a repressive element different from that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 VFEHMEQCAVKLAKMYGYVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPCTEMVADVNLP
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                   14;
                                                                                                                                                                                   Indels
PS50980; COA_CT_NTER; 1.
PS00866; CPSARE_1; 1.
PS00867; CPSARE_2; UNKNOWN 1.
2345 AA; 265121 MW; D48384CECCF6C7D8 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Acetyl-CoA carboxylase 1 (RC 6.4.1.2) (ACC-alpha)
                                                                                                                                                                                79; Mismatches 105;
                                                                                                                                 61.1%; Score 1776; DB 2; 63.4%; Pred. No. 6.4e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acetyl-CoA carboxylase 1 (EC 6.4 carboxylase (EC 6.3.4.14)].
Name=ACACA; Synonyms=ACAC, ACCA;
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                                                                                                                                                                             Matches 343; Conservative
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                                                                                                                                                          Similarity
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                                                                           LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                                              221
                                                                                                                                                LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGI----KETMMSDQGF 197
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                             ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIBFTVMATPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
                                                                                              LTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL
                                                                                                                                                                                                                                                                                                                                                                318 DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                    PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 TAENPOTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 RKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIODRLTAERPPADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis of long-chain fatty acids. This protein carries three functions: biotin carboxyl carrier protein, biotin carboxylase, and carboxyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin carboxylase (EC 6.3.1.14)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Finn-Dorset; TISSUE-Adipose tissue;
MEDLINE-95197015; PubMed-7890176; DOI=10.1016/0378-1119(94)00871-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=ACACA; Synonyms=ACAC;
Ovis aries (Sheep).
Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barber M.C., Travers M.T.;
Cloning and characterisation of multiple acetyl-CoA carboxylase
transcripts in ovine adipose tissue.";
Gene 154:271-275(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            + malonyl-CoA.
-!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein +
= ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 AV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    632
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                                        103
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                                                                                                              162
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         22
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Q285<u>5</u>9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COA1_SHEEP
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COFACTOR: Biotin.
ENZYME REGULATION: By phosphorylation (By similarity).
PATHWAY: Long-chain fatty acid biosynthesis, first (rate-limiting)
                                                                                                                                                            ADP + phosphate + carboxybiotin-carboxyl-carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.
Biotin (covalent) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00188; BIOILIN, 1.
PSS0968; BIOTINYL_LIPOYL; 1.
PSS0989; COA_CT_CTER; 1.
PSS0980; COA_CT_NTER; 1.
PS00966; CPSASE_1; 1.
PS00967; CPSASE_2; 1.
Ing; Biotin; Fatty acid biosynthesis; Ligase; Lipid ctional enzyme; Nucleotide-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coenzyme A (By similarity).
Coenzyme A (By similarity).
Coenzyme A (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Contains 1 ATP-grasp domain.
SIMILARITY: Contains 1 biotin carboxylation domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
SIMILARITY: Contains 1 carboxyltransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphoserine (By similarit MW; .32886C5D03EEAE0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carboxyltransferase.
ATP (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1775; DB 1;
Pred. No. 7.5e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biotinyl/lipoyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-grasp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR011762; COA_CT_N.
InterPro; IPR005481; CPA=C_L N.
InterPro; IPR005479; CPSase D2_ATP_bd.
Pfam; PF02785; Biotin_carb_C; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biotin_carb_C.
Biotin_lipoyl.
Carboxyl_trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ132890; CAB56826.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01039; Carboxyl_trans; 1.
Pfam; PF00289; CPSase L_chain; 1.
Pfam; PF02786; CPSase L_D2; 1.
PROSITE; PS50975; ATP GRASP; 1.
PROSITE; PS50979; BC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lipovl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nterPro, IPR011761, ATP_GRASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biotin BS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00188; BIOTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interPro; IPR011763; COA CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005482;
InterPro; IPR000089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Biotin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR011764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001882;
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1201
2346
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                                                                                                                                                                             COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      000955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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BINDING
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SEQUENCE
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NP_BIND
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CO (5)

-!- COFACTOR: Biotin

9

Gaps

16;

Indels

103;

Mismatches

78;

Conservative

Local Similarity

Best Local Sim Matches 345;

317

437

497 570 557

457

630

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LTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL 257
                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                          399 AVFEHMEQCAVKLARMVGYVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPCTEMVADVNL
                                                                                                                                                                                                                                                                                                             GEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPE
                                                                                                                                                         318 DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI
                                                                                                                                                                                                                        378 PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRI
                                                                                                                                                                                                                                            438 TAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEA
                                                                                                                                                                                                                                                                                                                                                            498 RKOWVISLKELSIRGDFRITVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissub=Heart;

Plassub=Heart;

Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

RemBl; AJS75431; CARGA140.2; "RRNA.

RMBL; AJS75431; CARGA140.2; "RRNA.

RGO; GO:0003999; F:acetyl-CoA carboxylase activity; IEA.

GO; GO:0001852; F:arp binding; IEA.

GO; GO:0001852; F:ATP binding; IEA.

RGO; GO:0001852; F:BTP CRASP.

R InterPro; IPR011761; ATP-GRASP.

R InterPro; IPR011761; ATP-GRASP.

R InterPro; IPR00182; Biotin Carb C.

InterPro; IPR005482; Biotin Lipoyl.

R InterPro; IPR005481; CPase L.

R InterPro; IPR005481; CPase L.

R InterPro; IPR005481; CPase L.

R InterPro; IPR005481; CPase L.

R InterPro; IPR005481; CPase L.

R InterPro; IPR005114; HPT-GerP.

R InterPro; IPR005114; HPT-GerP.

R InterPro; IPR005114; HPT-GerP.

R InterPro; IPR005114; HPT-GerP.

R InterPro; IPR005114; HPT-GerP.

R InterPro; IPR005114; HPT-GerP.

R InterPro; IPR005114; HPT-GerP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Acetyl-CoA carboxylase 2 (EC 6.4.1.2) (Fragment).
Name=ACACB;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fram; PP02785; Biotin carb C; 1.

Pfam; PP00284; Biotin lipoyl; 1.

Pfam; PP00289; CPSase L chain; 1.

PROSITE; PS50975; ATP GRASP; 1.

PROSITE; PS50975; BC; 1.

PROSITE; PS50976; BOTINI LIPOYL; 1.

PROSITE; PS50966; CPSASE 1; UNKNOWN 1.

PROSITE; PS00866; CPSASE 1; UNKNOWN 1.

PROSITE; PS00867; CPSASE 2; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 33
Q6KE89 HUMAN
ID Q6KE89 HUMAN PRELIMINARY;
AC Q6KE89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGI----KETWMSDQGF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |---KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSGSGLCVDWHENDFSKR-1 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSGU860; CECALE, 1.
PROSITE; PSGU867; CPSASE 2; 1.
ATP-binding; Biotin; Fatty acid biosynthesis; Ligase; Lipid synthesis; Multinctional enzyme; Nucleotide-binding; Phosphorylation.
Multifunctional enzyme; Nucleotide-binding; Phosphorylation.
 ENZYME REGULATION: By phosphorylation (By similarity).
PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.1%; Score 1775; DB 1; Length 2346; 63.7%; Pred. No. 7.5e-112; ive 77; Mismatches 104; Indels 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coenzyme A (By similarity).
Coenzyme A (By similarity).
Coenzyme A (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
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                                                             SIMILARITY: Contains 1 ATP-grasp domain.
SIMILARITY: Contains 1 biotin carboxylation domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCA010ADF6CD24EF
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Biotinyl/lipoyl.
Carboxyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity
                                                                                                                                                                                                                                                                                                                InterPro; IRR01882; Biotin BS.
InterPro; IRR001882; Biotin BS.
InterPro; IRR001089; Biotin Tarboyl.
InterPro; IRR001003; Carboxyl trans.
InterPro; IRR011763; COA CT C.
InterPro; IRR011763; COA CT C.
InterPro; IRR011763; COA CT N.
InterPro; IRR015479; CPSASE D2 ATP D6
Pfam; PF02785; Biotin Carb C; I.
Pfam; PF001039; Biotin Lipoyl; I.
Pfam; PF001039; CPSASE L-Chain; I.
Pfam; PF00289; CPSASE L-Chain; I.
PROSITE; PS50975; ATP GRASP; I.
PROSITE; PS50975; ATP GRASP; I.
PROSITE; PS50989; BIOTIN; I.
PROSITE; PS50989; COA CT CTER; I.
PROSITE; PS50989; COA CT CTER; I.
PROSITE; PS50989; COA CT CTER; I.
PROSITE; PS50989; COA CT CTER; I.
PROSITE; PS50989; COA CT CTER; I.
                                               SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                   EMBL; X80045; CAA56352.1; -; mRNA.
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                                                                                                                                                                                                                                                                                  InterPro, IPR011761, ATP_GRASP.
InterPro, IPR011764, BC.
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Best Local Similarity 63.77
Matches 345; Conservative
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2194
320
441
786
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BINDING
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MOD_RES
SEQUENCE
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DOMAIN
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Similarity
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Best Local Simi]
Matches 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                       Gaps
                              60.9%; Score 1769.5; DB 2; Length 1098; llarity 63.4%; Pred. No. 6.4e-112; Conservative 75; Mismatches 107; Indels 17;
 C2EA0759B6180AB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peng X.R., Lindgren K., Cornellussen B.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AJ575592, CAR01471.3; -; mRNA.
GO; GO:00003943; C:biotin carboxylase complex; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004075; F:biotin carboxylase activity; IEA.
GO; GO:001674; F:Digase activity; IEA.
GO; GO:001677; F:Digase activity; IEA.
GO; GO:001677; F:Digase activity; IEA.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Acetyl-CoA carboxylase 2 (EC 6.4.1.2).
Name=ACACB;
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 120931 MW;
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QEKEB7;
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NUCLEOTIDE SEQUENCE
                                              Best Local Similarity
Matches 344, Conserv
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.9%; Score 1769.5; DB 2; 63.4%; Pred. No. 1.9e-111; ive 75; Mismatches 107;
InterPro; IPR011764; AL.
InterPro; IPR011764; AL.
InterPro; IPR0011764; Biotin carb C.
InterPro; IPR001029; Biotin lipoyl.
InterPro; IPR011763; COA_CT_C.
InterPro; IPR011763; COA_CT_C.
InterPro; IPR011762; COA_CT_C.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR001481; Cphp_Synth_L_D2.
InterPro; IPR001481; Cphp_Synth_L_D2.
InterPro; IPR00149; Cphp_Synth_L_D2.
InterPro; IPR00149; Cphp_Synth_L_D2.
InterPro; IPR00149; Cphp_Synth_L_D2.
InterPro; IPR00149; Cphp_Synth_L_D2.
InterPro; IPR00184; Biotin_lipoyl; I.
Pfam; PF00189; Cpsase_L_chain; I.
PROSITE; PS50975; ATP_GRASP; I.
PROSITE; PS50989; COA_CT_CTER; I.
PROSITE; PS50989; COA_CT_CTER; I.
PROSITE; PS00866; CPSASE_I; UNKNOWN I.
PROSITE; PS00866; CPSASE_I; UNKNOWN_I.
PROSITE; PS00867; CPSASE_I; UNKNOWN_I.
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us-10-633-835-2.rup

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542 AIFERMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL 600
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                                                                                                                                                   PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKT-QRKPQPQGHVVACR
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Eukaryota; Metazoa; Arthopoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;

Anophelinae; Anopheles.

NCBI_TAXID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=PEST;
The Anopheles gambiae Sequence Committee;
"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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EMBL; AAAB01008900; EAA09449.3; -; Genomic_DNA
GO; GO:0005524; F:ATP binding; IEA.
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GO; GO:0016874; F:liqase activity; IEA.
GO; GO:0008152; F:metabolism; IEA.
InterPro; IPR011761; ATP GRASP.
InterPro; IPR011764; BC.
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InterPro; IPRO11763; COA_CT_C.
InterPro; IPRO11762; COA_CT_N.
InterPro; IPRO05491; CPARE L.N.
InterPro; IPRO05479; Cphp synth L.D2.
Pfan; PPO0364; Biotin_lipoyl; 1.
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InterPro; IPR005482; Biotin_carb_C.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000022; Carboxyl_trans.
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ORFNames=ENSANGG0000013173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O7PO11_ANOGA PRELIMINARY;
07P011;
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NUCLEOTIDE SEQUENCE.
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07PQ11 ANOGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QGFL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 GEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541
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                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 LC--KNGVAFLGPPSEAMWALGDKIASTVVAQTLQVPTLPWSGSGLTVEWTEDDLQQGKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maco J., Wakil S.J.;

Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

R Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0009343; C:biotin carboxylase complex; IEA.

GO; GO:000989; F:acetyl-CoA carboxylase activity; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004075; F:biotin carboxylase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

R GO; GO:0008152; P:metabolism; IEA.

R InterPro; IPR011764; BC:

R InterPro; IPR001764; BC:

R InterPro; IPR001764; Biotin_carb_C.

R InterPro; IPR001764; Biotin_lapyl.

R InterPro; IPR001764; Carboxyl_trans.

R InterPro; IPR011763; CAB_CT_N.

R InterPro; IPR011763; CAB_CT_N.

R InterPro; IPR011763; COA_CT_C.

R InterPro; IPR001763; Caba_CT_N.

R InterPro; IPR001763; Caba_CT_N.

R InterPro; IPR001763; CAB_CT_N.

R InterPro; IPR001764; CAB_CT_N.

R InterPro; IPR001764; CAB_CT_N.

R InterPro; IPR001764; CAB_CT_N.

R InterPro; IPR001764; CAB_CT_N.

R InterPro; IPR001764; CAB_CT_N.

R InterPro; IPR001764; CAB_CT_N.

R InterPro; IPR001764; CAB_CT_N.

R InterPro; IPR001764; CAB_CT_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2458 AA; 276539 MW; 08C54086D5B2DC16 CRC64;
                                                                                          05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Acetyl-CoA carboxylase 2 (EC 6.4.1.2).
PRT; 2458 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50989; COA_CT_CTER; 1.
PS50980; COA_CT_NTER; 1.
PS50086; CPSĀSE_1; UNKNOWN 1.
PS00867; CPSĀSE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01039; Carboxyl_trans; 1.
PF00289; CPSase_L_chain; 1.
PF02786; CPSase_L_D2; 1.
IE; PSS0975; ATP_GRASP; 1.
IE; PSS0979; BC; 1.
                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ); Carboxyl fra-
Q6TY48_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Heart;
                                                                                                                                                                                            Name=ACC2;
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AC Q4RSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                      --HKKNLVPLGPPERAMMALGDKVASSIVĄQTAEIPTLPWSGSELKAQYSGKK--IKISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 612
                                                                                                                                                                                                                                                                           KVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESL
                                                                                                                                                                                                                                                                                                                                                                                                                  AASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENP
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                                                                                                                                                                                                                                                      SPVADPIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDL
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIODRLTAERPPADLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Terrandon nigroviridis (Green puffer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Meopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetraodontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                12;
                                                                                                                                                                         Length 2314;
                                                                                                                                                                                                                Indels
                                                                                                                                260424 MW; E069582640C66B08 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAF14650, whole genome shotgun sequence.
ORFNames=GSTENG00020334001;
                                                                                                                                                                       60.8%; Score 1767; DB 2;
63.3%; Pred. No. 2.6e-111;
cive 76; Mismatches 109;
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              COA_CT_CTER; 1.
COA_CT_NTER; 1.
COSASE_1; 1.
CPSASE_2; UNKNOWN_1.
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Conservative 7
  BIOTINYL
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Q4SCU3;
                                                                                                                                2314 AA;
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                                                                                                                                                                                             Similarity
                  PS50989;
PS50980;
PS50968;
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                                                                                                                NON TER
SEQUENCE
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                                                       PROSITE;
PROSITE;
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                PROSITE;
PROSITE;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ASPVADFIRKOGGHSVITKVLLCNNGIAAVKEIRSIBKMAYETFGDERALEFTVMATPED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 SGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKI
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Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak Kells M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; Genome duplication in the teleost fish Tetraodon nigroviridis rev the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                     which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1267;
                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                            preliminary data.
, CAAE01014650; CAG01539.1; -; Genomic DNA.
ENCE 1267 AA; 141834 MW; 682ADAAE28A169F6
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.4%; Score 1757; DB 2;
Best Local Similarity 57.7%; Pred. No. 5.5e-111;
Matches 350; Conservative 69; Mismatches 106;
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64 NAEYIRWADQILQVPGGSNNNNYANVDIIVDFAERAGVQAVWAGWGHASENPRLPDLLSK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sucgang R., Berriman M., Song J., Olsen R., Safranski K., Xu Q., Sucgang R., Berriman M., Song J., Olsen R., Safranski K., Xu Q., Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F., Bankier A.T., Chem G., Saunders D., Sodergren B., Davis P., Pilcher K., Chen G., Saunders D., Sodergren B., Davis P., Rerbornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N., A parbrother P., Desany B., Just B., Morio T., Rost R., Churcher C., Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I., Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R., Mardroper A., Felder M., Thangavelu M., Johnson D., Knights A., Loulseged H., Mungall K., Oliver K., Price C., Quail M.A., Loulseged H., Mungall K., Oliver K., Price C., Quail M.A., Mr. Hernandez J., Rabbinowitsch E., Steffen D., Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A., Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y., Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C., Millams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A., The genome of the social amoeba Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 INEYIKKLGGDKNIEKILIANNGIAAVKAIRSVRKWAYTNFGNERAIKFVVMATPEDMKA
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                                                        STSTWGYPSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEY
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Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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BDBEA99629EE1B2B CRC64;
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-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry
                                                                                                                                  LIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV 559
                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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LIKLLETESFRSNEIDTGWLDYLIAEKVQAERPDTMLGI
                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                                                                                                                                                                                         Last annotation
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Last sequence
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Name=accA; ORFNames=DDB0230067;
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                                                                                                                                                                                                                                                               DICDI PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEIGYPVVIKASEGGGGGKGIRKVENSEDFPGFFRQVQSEAPGSPIFIMQLAQHARHLEVQ 324
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|VDIAKRIPVQVLCSLTFRAVWAGWGHASENPKLPELL--DKAGISFLGPSSKAMWALGD
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                                                                                             Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthomorpha, Acanthopterygii, Percomorpha; Tetraodontiformes, Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 12 SCAF14999, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.0%; Score 1716; DB 2; 158.9%; Pred. No. 8.1e-108; ive 73; Mismatches 113;
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                                                                            ORFNames=GSTENG00029540001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 431:946-957 (2004).
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                                                 KAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQV 384
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VFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESME 324
                                                                                                                                                                                                                    MVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV 559
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98322122; PubMed=9655932; DOI=10.1016/S0167-4781(98)00060-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abe K., Shinohara Y., Terada H.; "Isolation and characterization of cDNA encoding rat muscle type acetyl-CoA carboxylase."; Biochim. Biophys. Acta 1398:347-352(1998).
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004075; F:biotin carboxylase activity; IEA.
GO; GO:0016674; F:liase activity; IEA.
GO; GO:0016152; P:metabolism; IEA.
InterPro; IPR011761; ATP GRASP.
InterPro; IPR011764; BC.
InterPro; IPR000849; Biotin carb C.
InterPro; IPR000899; Biotin lipoyl.
InterPro; IPR000089; Biotin lipoyl.
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Last annotation update)
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P; Q00955; 1004.
embl; ENSRNOG000000000658; Rattus norvegicus.
; 620500; Acacb.
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InterPro; IPR011763; COA_CT_N.
InterPro; IPR005481; CPASE_LN.
InterPro; IPR005149; Cphg_Synth_L_D2.
InterPro; IPR005114; HPr_SerP_S.
Pfam; PP02785; Biotin_Carb_C; I.
Pfam; PP01039; Carboxyl trans; I.
Pfam; PP01039; Carboxyl trans; I.
Pfam; PP00289; CPSase_L_Chain; I.
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PS50989; COA_CT_CTER; 1.
PS50980; COA_CT_NTER; 1.
PS00866; CPSASE_1; UNKNOWN_1
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Carboxyl_trans.
COA_CT_C.
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Name=Acacb;
Rattus norvegicus (Rat)
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PS00867; CPSASE 2; UNKNOWN 1.
PS00589; PTS HPR SER; UNKNOWN 1.
2456 AA; 276098 MW; C1D41AF0BEA38863 CRC64;
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                                                                                                  Query Match 57.6%; Score 1673.5; DB 2; Best Local Similarity 60.2%; Pred. No. 6.9e-105; Matches 327; Conservative 78; Mismatches 121;
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Job time: 253 secs
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 PPPDHKAVSQFIGGNPLETA........DGLIQDRLTAERPPADLAV 559
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-633-835-26
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Seguence 8, Appli	199		Sequence 32, Appl	Sequence 44, Appl	Sequence 38, Appl	Sequence 43, Appl	Sequence 65, Appl	37,	45,	39,	46,	Sequence 66, Appl		40,	68	67.	Sequence 69, Appl
US-10-633-835-8	US-10-369-493-1998	US-10-633-835-36	US-10-633-835-32	US-10-633-835-44	US-10-633-835-38	US-10-633-835-43	US-10-633-835-65	US-10-633-835-37	US-10-633-835-45	US-10-633-835-39	US-10-633-835-46	US-10-633-835-66	US-10-633-835-47	US-10-633-835-40	US-10-633-835-68	US-10-633-835-67	US-10-633-835-69
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70.9	70.9	70.8	70.7	9.02	70.6	9.02	70.4	70.3	6.69	6.69	69.7	69.5	69.1	69.1	9.89	67.9	67.7
2060	2060	2058.5	2054	2051	2051	2051	2046	2042.5	2033	2033	2026	2020	2009	2009	1994.5	1973	1967.5
28	58	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

SEQUENCE 2, Application US/10633835

SEQUENCE 2, Application NG/10633835

SEQUENCE 2, Application NG/10633835

SEQUENCE 3, VOLTATE 10 NG/10633835

SEQUENCE 3, VOLTATE 10 NG/1086994A1

SEPPLICANT: Weatherly, Sandra L.

TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SEQ ID NO 2

LENGTH: 559

TYPE: PRIT

SEQ ID NO 2

LENGTH: 559

TYPE: PRIT

CORGANISM: Ustilago maydis

US-10-633-835-2

Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 3e-254;

Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps

61 AYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERA 120 61 AYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERA 120 121 GVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCM 180 240 240 300 241 RKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQ 300 9 1 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKW 1 PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKW 241 RKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQ 181 PWSGTGIKETWMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGI 181 PWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGI ò ò g 8 셤 Š 셤 ò g

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301 RRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP

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Sequence 27, Application US/10633835
Fublication No. US20040086994A1
Fublication No. US20040086994A1
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Fublication No. US20040086994A1
Fublication No. US20040A1
Fublication NUMBER: US/10/633,835
FUBLERFERENCES 9280. 2003-08-04
FUBLERFILING DATE: 2003-08-04
FRIOR FILING DATE: 2003-08-05
FRIOR FILING DATE: 2003-08-05
FRIOR FILING DATE: 2003-08-05
FRIOR FULL OF SEQ ID NOS: 71
SEQ ID NO 27
FUBLERFILING DATE: 2003-08-05
FRIOR FULL SEQ ID NOS: 71
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FRIOR FULL SEQ ID NOS: 71
FRIENDERFERENCES PARENCES PARENCES FARENCES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1). [554)
CTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAs 4-547)
US-10-633-835-27
540
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Sequence 23, Application US/10633835

Fublication No. US20040086994A1

Fublication No. US20040086994A1

FRENERAL INFORMATION:

APPLICANT: Elich, Tedd D.

APPLICANT: Volrath, Sandra L.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL Coa Carboxylase INHIBITORS

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT APPLICATION NUMBER: US 60/401,170

FRIOR PRILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin Version 3.2

LENGTH: 549
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OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC domain (AAs 2-550)
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100.0%; Pred. No. 1e-249;
iive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 549; Conservative
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NAME/KEY: MISC_FEATURE
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Publication No. US20040086994A1
GENERAL INFORMATION:
APPLICANT: Elich, Tedd D.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
CURRENT APPLICATION UNMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SSOTUMER PATENTION OF SEQ ID NOS: 71
SSOTUMER PATENTION OF SEQ ID NOS: 71
SSOTUMENT OF SEQ ID NOS: 71
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. OTHER INFORMATION: N-terminal deleted Ustilago ACCase BC domain (AAs US-10-633-835-17
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98.8%; Score 2872; DB 4; I
Best Local Similarity 100.0%; Pred. No. 4.4e-251;
Matches 554; Conservative 0; Mismatches 0;
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ORGANISM: Ustilago maydis
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US-10-633-835-17
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; LOCATION: (1). [549)
; OTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAS 7-555)
US-10-633-835-28
                                                                                                                                                                                                                                                                                        Sequence 28, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
APPLICANT: Bitch. Tedd D.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: ACETYL CAA CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TILE OF INVENTION: ACETYL CAA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
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                  421 HVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAY
                                                                            GADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIODRLTA
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Best Local Similarity 100.
Matches 549; Conservative
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TYPE: PRT
ORGANISM: Ustilago maydis
                                                                                                                                                       ERPPADLAY 559
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Sequence 18, Application US/10633835
Sequence 18, Application US/10633835
Publication No. US20040086994A1
Sequence 18, Application US/10633835
APPLICANT: Elich, Tedd D.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION NUMBER: US/10/633,835
CURRENT APPLICATION NUMBER: US 60/401,170
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR APPLICATION NUMBER: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SSOFTWARE: Patentin version 3.2
LENGTH: 549
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NAME/KEY: MISC FEATURE
LOCATION: (1)...(549)
COTHER INFORMATION: N-terminal deleted Ustilago ACCase BC domain (AAs 12-560)
US-10-633-835-18
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                                       61 IEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWG
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Best Local Similarity 100.(
Matches 549; Conservative
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ORGANISM: Ustilago maydis
                                                                                                                                                                                               DGLIQDRLT 549
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NAME/KEY: MISC FEATURE LOCATION: (1)...(539)
COTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAs 12-550 US-10-633-835-29
                                                                                                                                                                                APPLICANT: Blich, Tedd D.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US 60/401,170
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR PILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 539
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       KTQRKPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480
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                                                                                                          RESULT 9
US-10-633-835-29
'Sequence 29, Application US/10633835
'Publication No. US20040086994A1
'GENERAL INFORMATION'
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Ustilago maydis
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Best Local Similarity
Matches 539; Conserv
       421
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                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE
; LOCATION: (1)...(539)
; CTHER INFORMATION: C-terminal deleted Ustilago ACCase BC domain (AAs 2-540)
US-10-633-835-24
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                                                           HIFAYGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQ 545
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larity 100.0%; Pred. No. 2.7e-245;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                              Sequence 24, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
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nes 539; Conserva
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US-10-633-835-24
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APPLICANT: Elich, Tedd D.
APPLICANT: Blich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION (TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT PILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR APPLICATION NUMBER: US 60/401,170
SOFTWARE OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 25
LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC_FEATURE

1 LOCATION: (1)...(529)

9 OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC domain (AAs 2-530)

US-10-633-835-25
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100.0%; Pred. No. 3.9e-240;
ive 0; Mismatches 0;
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Publication No. US20040086994A1
GENERAL INFORMATION:
APPLICANT: Blich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
US20040086994A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 529; Conservative
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US-10-633-835-30
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                                                                                             Sequence 19, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF;
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ 1D NOS: 71
; SOUTHARE: Patentin version 3.2
; SEQ 1D NO 19
; LENTER ELICH OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR OF TELLOR 
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COTHER INFORMATION: N-terminal deleted Ustilago ACCse BC domain (AAs 22-560)
US-10-633-835-19
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Best Local Similarity 100.0%; Pred. No. 2.7e-244;
Matches 539; Conservative 0; Mismatches 0;
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ORGANISM: Ustilago maydis
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RESULT 11 US-10-633-835-25 ; Sequence 25, Application US/10633835

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us-10-633-835-2.rapbm

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APPLICANT: Elich, Tedd D.
APPLICANT: Blich, Tedd D.
APPLICANT: Wolzath, Sandra L.
APPLICANT: Wolzath, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REPERROCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR PLING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 26
                                                                                                                                                                                                        ; LOCATION: (1). [529)
; OTHER INFORMATION: N-terminal deleted Ustilago ACCase BC domain (AAs 32-560)
US-10-633-835-20
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                                                                                                                                                                                                                                                                                                           94.5%; Score 2746; DB 4; I 100.0%; Pred. No. 1.1e-239; iive 0; Mismatches 0;
             60/401,170
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Publication No. US20040086994A1
GENERAL INFORMATION:
      PRIOR APPLICATION NUMBER: US 6(PRIOR FILING DATE: 2003-08-05 NUMBER OF SEQ ID NOS: 71 SOFTWARE: PATENTIN VERSION 3.2 SEQ ID NO 20 LENGTH: 529
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 529; Conservative
                                                                                                                                   TYPE: PRT
ORGANISM: Ustilago maydis
                                                                                                                                                                         FEATURE:
NAME/KEY: MISC FEATURE
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. OTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAs 17-545)
US-10-633-835-30
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REPERENCE: 9280.2
CURRENT PAPLICATION NUMBER: US/10/613,835
CURRENT APPLICATION NUMBER: US 60/401,170
PRIOR RAPLICATION NUMBER: US 60/401,170
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VETSION 3.2
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; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOWAINS FOR IDENTIFICATION OF
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT PILING DATE: 2003-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 MATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASEN 135
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100.0%; Pred. No. 9e-240;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 529; Conservative
                                                                                                                                                                                                                                                          ORGANISM: Ustilago maydis
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US-10-633-835-20
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LOCATION: (1)..(519)
OTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAS 22-540
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                                                                             Length 519;
                                                                                                                Indels
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, OTHER INFORMATION: N-terminal deleted Ustilago ACCase BC
US-10-633-835-21
                                                                         Score 2698; DB 4; L
Pred. No. 2.4e-235;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 21, Application US/10633835; Publication No. US20040086994A1; GENERAL INFORMATION:
                                                                         Query Match
92.8%; Soc
Best Local Similarity 100.0%; P:
Matches 519; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.78;
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ORGANISM: Ustilago maydis
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                    ; OTHER INFORMU
US-10-633-835-31
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Publication No. US20040086994a1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blich, Tedd D.
APPLICANT: Weatherly, Stephanie C.
APPLICANT: Weatherly, Stephanie C.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT PAPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-05
PRIOR FILING DATE: 2003-08-05
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| NAME/KEY: MISC FEATURE |
| LOCATION: (1). [519] |
| OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC domain (AAs2-520) |
| US-10-633-835-26
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                                                                                                                                                                     Query Match 93.0%; Score 2703; DB 4; Length 519; Best Local Similarity 100.0%; Pred. No. 8.5e-236; Matches 519; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Patentin version 3.2
SEQ ID NO 31
LENGTH: 519
              TYPE: PRT
ORGANISM: Ustilago maydis
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NAME/KEY: MISC_FEATURE
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APPLICANT: Blich, Tedd D.
APPLICANT: Blich, Tedd D.
APPLICANT: Blich, Tedd D.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINATE BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 2.1
LENGTH: 519
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APPLICANT: Blich, Tedd D.
APPLICANT: Blich, Tedd D.
APPLICANT: Weatherly, Sandra L.
APPLICANT: Weatherly, Stephanie C.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US /10/633,835
CURRENT FILING DATE: 2003-08-05
FRIOR PLLING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 5.2
LENGTH: 581
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NAME/KEY: MISC_FEATURE
LOCATION: (1)...[581)
OTHER INFORMATION: N-terminal deleted Magnaporthe ACCase BC domain (AAs 12-592
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                                                                                                                   VWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSG
         HKIADHFIGGNRLENAPPSKVKEWVAAHDGHTVITNVLIANNGIAAVKEIRSVRKWAYET
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Publication No. US20040086994A1
GENERAL INFORMATION:
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Matches 408; Conservative
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US-10-633-835-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Elich, Tedd D.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Wolrath, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION (TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT PILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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   5.6e-235;
                   Mismatches
   Pred.
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"Sequence 53, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
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ORGANISM: Magnaporthe grisea
                 519; Conservative
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Best Local Similarity 73.5
Matches 408; Conservative
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 Best Local Similarity
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                 VWAGWGHASENPKLPESLAASPKKIIFIGPPGSAMRSLGDKISSTIVAQHAQVPCIPWSG
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Fublication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLAN

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR PILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 3698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)..(2301)
; OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-3698
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ORGANISM: Neurospora crassa
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US-10-369-493-3698
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; Bublication No. US20040086994A1
; GENERAL INFORMATION:
    APPLICANT: Elich, Tedd D.
    APPLICANT: Weatherly, Stephanie C.
    TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
    TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
    FILE REFERENCE: 9280.2
    CURRENT APPLICATION NUMBER: US/10/633,835
    CURRENT APPLICATION NUMBER: US 60/401,170
    PRIOR FILING DATE: 2003-08-05
    NUMBER OF SEQ ID NOS: 71
    SOFTWARE: Patentin version 3.2
    SEQ ID NO 6
    LENGTH: 591
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; ORGANISM: Magnaporthe grisea
US-10-633-835-6
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Best Local Similarity 73.5
Matches 408; Conservative
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US-10-633-835-6
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Sequence 55, Application US/10633835;
Publication No. US20040086994A1
GENERAL INFORMATION:
APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOWAINS FOR IDENTIFICATION OF
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT PILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOOFWARE: PATENTIN VERSION 3.2
SEQ ID NO 55
LENGTH: 571
   217 IGVDAVQIDKKGIVTVDDDTYAKGCVTSWQEGLEKARQIGFPVMIKASEGGGGKGIRKAV 276
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                                                                                                                                                 277 SEEGFEELYKAAASEIPGSPIFIMKLAGNARHLEVQLLADQYGNNISLFGRDCSVQRRHQ 336
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PEATURE:
NAME/KEY: MISC_PEATURE
LOCATION: (1)...(571)
OTHER INFORMATION: C-terminal deleted Magnaporthe ACCase BC domain (AAs US-10-633-835-55
                                                         TGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCT
                                                                                                                            245 NGEEFKQLYNAVLGEVPGSPVFVMKCAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHO
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73.8%; Pred. No. 7.4e-182;
iive 58; Mismatches 82;
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Best Local Similarity 73.8%
Matches 395; Conservative
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APPLICANT: Wolrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION (
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REPERENCE: 9280.2
FILE REPERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR PAPLICATION NUMBER: US 60/401,170
PRIOR PLICATION NUMBER: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 54
LENGTH: 581
                                                                                                                                                            QVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENP 442
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                                                                   AASKHKIIPIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSD
                                                                                                                                         DVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPG
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OTHER INFORMATION: C-terminal deleted Magnaporthe ACCase (AAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.4%; Score 2135; DB 4; Length 581;
llarity 73.6%; Pred. No. 3.3e-184;
Conservative 59; Mismatches 85; Indels
NNNYANVDLIVDVAERAGVHAVWAGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 54, Application US/10633835; Publication No. US20040086994A1; GENERAL INFORMATION:
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72-592)
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APPLICANT: Elich, Sandra L.
APPLICANT: Volrath, Sandra L.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TILE REFERENCE: 2003-08-04
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
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; LOCATION: (1)...(521)
; OTHER INFORMATION: N-terminal deleted Magnaporthe ACCase BC domain (AAs
US-10-633-835-64
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                                                                                                         TTEMVSGVNLPAAQLQVAMGLPLSRIPHIRELYGLPRDGDSEIDFFFQNPESFKVQKVPT
                                                                                                                                                                  FAYGADRSEARKOMVISLKELSIRGDFRTTVBYLIKLLETDAFESNKITTGWLDGLIQDR
                            EEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHP
                                                       EEAPVTIAPAATFHEMERAAVRLGELVGYASAGTIEYLYEPENDRFYFLELNPRLOVEHP
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Pred. No. 9.6e-179;
5; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                               Sequence 64, Application US/10633835 Publication No. US20040086994A1 GENERAL INFORMATION:
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75.0%; Predictive 55; I
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ORGANISM: Magnaporthe grisea
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Best Local Similarity 75.0%
Matches 391; Conservative
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541 VTSARPDKMLAV 552
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APPLICANT: Gao. Yongwei
APPLICANT: Gao. Yongwei
APPLICANT: Gater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
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APPLICANT: Goldman, Barry S.
APPLICANT: SAPPLICANTON: PLANTS WITH IMPROVED PROPERTIES
FILLE REFERENCE: 38-10(5-505.2)8
FRIOR FILING DATE: 2003-02-28
FRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2130
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   157 VWAGWGHASENPKLPESLAASPKKIIFIGPPGSAMRSLGDKISSTIVAQHAQVPCIPWSG 216
                                                  NGEEFKQLYNAVLGEVPGSPVFVWKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQ 304
                                                                                                          KIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364
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                                                                                                                                                                                                                EHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQR
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Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Schizosaccharomyces pombe
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GENERAL INFORMATION:
APPLICANT: Blich, Tedd D.
APPLICANT: Wolrath, Sanda L.
APPLICANT: Workarion:
APPLICANT: Workarion:
TITLE OF INVENTION: ACETYL COA CARBOXYLASE DOMAINS FOR IDENTIFICATION OF
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT APPLICATION NUMBER: US 60/401,170
PRIOR PILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 34
LENGTH: 570
LENGTH: 570
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OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain
OTHER INFORMATION: 12-581)
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        RLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESF 420
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                                                                                         DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL
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US-10-633-835-34
; Sequence 34, Application US/10633835
; Publication No. US20040086994A1
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ORGANISM: Saccharomyces cerevisiae
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| DDLITHKMTAEKPDPTLAV 560
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US-10-633-835-34
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i Sequence 35, Application US/10633835

j Sequence 35, Application US/10633835

j Publication No. US20040086994A1

j Publication No. US20040086994A1

j APPLICANT: Blich, Tedd D.

j APPLICANT: Weatherly, Stephanie C.

j TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

j TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

j TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

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j TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

j TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

j CURRENT FILING DATE: 2003-08-04

j PRIOR APPLICATION NUMBER: US 60/401,170

j PRIOR PLING DATE: 2003-08-05

j SEQ ID NOS: 71

j SOFTWARE: Patentin version 3.2

j SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE
LOCATION: (1). (560)
COTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAstrones Information: 22-581)
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                                                                 LYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMGALTELNF
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                                                                                                                                                                                                       EYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV 559
                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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APPLICANT: Blich, Tedd D.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Wolrath, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT APPLICATION NUMBER: US 60/401,170
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR PLING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 71
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                   DSQFGHIPAYGADRSEARKQMYISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-633-835-8
                                                                                                                                                                                                                                                                                                                  ; Sequence 8, Application US/10633835; Publication No. US20040086994A1; GENERAL INFORMATION:
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DDLITHKMTAEKPOPTLAV 575
                                                                                                                                                                                                     DGLIQDRLTAERPPADLAV 559
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OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAS
OTHER INFORMATION: 7-591)
                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/10633835

Sequence 33, Application US/20040086994A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Elich, Tedd D.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: ACETYL COA CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR APPLICATION DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71

SOFTWARE: PATENTIN VETSION 3.2
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RLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESF 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.9%; Score 2060; DB 4; Length 575; llarity 69.1%; Pred. No. 2.1e-177; Conservative 76; Mismatches 89; Indels
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                                                                                                                                                                                                     DGLIQDRLTAERPPADLAV 559
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DDLITHKMTAEKPDPTLAV 570
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Best Local Similarity
Matches 386; Conserv?
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LENGTH: 575
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APPLICANT: Blich, Tedd D.
APPLICANT: Blich, Tedd D.
APPLICANT: Blich, Tedd D.
APPLICANT: Weatherly, Stephanie C.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REPERBNCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR PLLING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 36
LENGTH: 550
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          DSOFGHIFAYGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL
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OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase OTHER INFORMATION: 32-581
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Sequence 36, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
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Matches 384; Conservative
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Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Stater, Steven C.
APPLICANT: Stater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Ghldman, Barry S.
APPLICANT: Gridman,                                                501
                                                                                                                                                   561
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                                                                                                                         PDHKAVSQFIGGNPLETAPAS PVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAY
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70.9%; Score 2060; DB 4; Length 2233;
Best Local Similarity 69.1%; Pred. No. 1.7e-176;
Matches 386; Conservative 76; Mismatches 89; Indels 8
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DDLITHKMTAEKPDPTLAV 580
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ORGANISM:
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APPLICANT: Blich, Tedd D.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: ACETYL COA CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR PLILNG DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1). (570)
OTHER INFORMATION: N- and C-terminal deleted Saccharomyces cerevisiae ACCase OTHER INFORMATION: domain (AAs 7-576)
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                                                                                                                                                            ; Sequence 44, Application US/10633835; Publication No. US20040086994A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Sąccharomyces cerevisiae
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DDLITHKMTABKPDPTLAV
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Best Local Similarity 69.3%;
Matches 383; Conservative
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NAME/KEY: MISC FEATURE
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US-10-633-835-44
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US-10-633-835-44
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APPLICANT: Volrath, Sandra L.
APPLICANT: Volrath, Sandra L.
APPLICANT: Volrath, Stephanie C.
TITLE OF INVENTION: RECOMBINATE BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 32
LENGTH: 580
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AYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: MISC_FEATURE
; LOCATION: (76)...(76)
; OTHER INFORMATION: Saccharomyces cerevisiae ACCase BC domain S77Y
US-10-633-835-32
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70.7%; Score 2054; DB 4; Length 580;
Best Local Similarity 68.9%; Pred. No. 7.4e-177;
Matches 385; Conservative 76; Mismatches 90; Indels 8;
                                                                                                                                                                           ; Sequence 32, Application US/10633835; Publication No. US20040086994A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Saccharomyces cerevisiae
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APPLICANT: Blich, Tedd D.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Wolrath, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION C
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT PAPLICATION NUMBER: US 10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR PILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) LOCATION: (1). (575)
) OTHER INFORMATION: N- and C-terminal deleted Saccharomyces cerevisiae ACCase;
) OTHER INFORMATION: domain (AAs 4-578)
US-10-633-835-43
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      123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPW 182
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69.3%; Pred. No. 1.4e-176;
iive 76; Mismatches 86;
                                                                                                                                                                   ; Sequence 43, Application US/10633835; Publication No. US20040086994A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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Best Local Similarity 69.3*
Matches 383; Conservative
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OTHER INFORMATION: C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAS
OTHER INFORMATION: 2-576)
                                                                                                                                                         Sequence 38, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
APPLICANT: Bitch, Tedd D.
APPLICANT: Weatherly, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: APPLICANTION WHARER: US/10/633,835
CURRENT APPLICANTION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR APPLICATION DATE: 2003-08-05
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DDLITHKMTAEKP 569
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Matches 383; Conservative
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                                                                                                                              RESULT 33
US-10-633-835-38
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Sequence 37, Application US/10633835

Sequence 37, Application US/10633835

Sequence 37, Application US/10633835

Publication No. US20040086994A1

GENERAL INFORMATION:
APPLICANT: Blich, Tedd D.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: ACETYL COA CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT APPLICATION NUMBER: US 60/401,170

PRIOR APLICATION NUMBER: US 60/401,170

PRIOR PLING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.2

LENGTH: 540

TYPE: PRT
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COCATION: (1)...(540)
OTHER INFORMATION: N-terminal deleted Saccharomyces cerevisiae ACCase BC domain
OTHER INFORMATION: 42-581)
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182 DDDIYQKGCCTSPEDGLQKAKRIGFPVMIKASEGGGGKGIRQVEREEDFIALYHQAANBI
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ORGANISM: Saccharomyces cerevisiae
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US-10-633-835-37
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                                                                                                                                                                                                                                             Sequence 65, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
APPLICANT: Blich, Tedd D.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Wolrath, Sephanie C.
APPLICANT: Wolrath, Stephanie C.
APPLICANT: Wolrath, Stephanie C.
APPLICANT: Wolrath, Sephanie C.
APPLICANT: Wolrath, Stephanie C.
APPLICANT: Wolrath, S
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OTHER INFORMATION: N- and C-terminal deleted Magnaporthe ACCase OTHER INFORMATION: 72-582)
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Best Local Similarity 75.1%; Pred. No. 3.2e-176;
Matches 384; Conservative 55; Mismatches 72;
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ORGANISM: Magnaporthe grisea
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DDLITHKMTAEKP 572
                                                                            DGLIQDRLTAERP 553
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US-10-633-835-65
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LOCATION: (1). [570)
OTHER INFORMATION: C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (A OTHER INFORMATION: 2-571)
                                                                                 APPLICANT: Blich, Tedd D.
APPLICANT: Voltach, Sandra L.
APPLICANT: Voltach, Sandra L.
APPLICANT: Voltach, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TILLE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 39
LENGTH: 570
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                           Sequence 39, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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            Sequence 45, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: APPLICANTION NUMBER: US 60/401,170
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR APPLICATION NUMBER: US 60/401,170
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 45
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OTHER INFORMATION: N- and C-terminal deleted Saccharomyces cerevisiae ACCase OTHER INFORMATION: domain (AAs 12-571)
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Best Local Similarity 69.24
Matches 380; Conservative
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DDLITHKMT 560
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Sequence 66, Application US/10633835

Sequence 66, Application US/10633835

Publication No. US200400869941

GENERAL INPORMATION:
APPLICANT: Blich, Tedd D.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: ACETYL COA CARBOXYLASE DOMAINS FOR IDENTIFICATION OF:
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT FILING DATE: 2003-08-04

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin Version 3.2

SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
OTHER INFORMATION: N- and C-terminal deleted Magnaporthe ACCase BC domain (AAs
OTHER INFORMATION: 72-572)
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69.5%; Score 2020; DB 4; Length 5
Best Local Similarity 75.4%; Pred. No. 7.1e-174;
Matches 378; Conservative 54; Mismatches 69; Indels
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Job time : 187 secs
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US-10-633-835-66
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                                                                                                                    IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC_PEATURE

LOCATION: (1)... [550)

OTHER INFORMATION: N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC

J. OTHER INFORMATION: domain (AAs 17-566)
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          Sequence 46, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
APPLICANT: Elich, Tedd D.
APPLICANT: Wolrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FILE REFERENCE: 9280.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Best Local Similarity 69.7%; Pred. No. 2.3e-174;
Matches 379; Conservative 73; Mismatches 84;
                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR PILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 46
LENGTH: 550
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OM protein - protein search, using sw model

February 4, 2006, 18:25:41; Search time 16 Seconds (without alignments) 409.400 Million cell updates/sec Run on:

US-10-633-835-2 2907 1 PPPDHKAVSQFIGGNPLETA......LDGLIQDRLTAERPPADLAV 559 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

88029 segs, 11718060 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA New:\*

1: /cgn2\_6/ptodata/2/pubpaa/USO8\_NEW\_PUB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/USO7\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/USO7\_NEW\_PUB.pep:\*

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8: /cgn2\_6/ptodata/2/pubpaa/USIO\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/USIO\_NEW\_PUB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 14, Appl	16	Sequence 4, Appli	13	ω.	4	Sequence 11, Appl	60	10,	2,	710	1642			12,	13,		218,	804	648,	1654,	370, 7	Sequence 1002, Ap		Sequence 1000, Ap
SUMMAKIES	ID	US-11-186-999-14	US-11-186-999-16	US-11-144-368-4	US-11-186-999-13	US-11-186-999-6	US-11-186-999-4	US-11-186-999-11	US-11-186-999-8	US-11-186-999-10	US-11-186-999-2	US-10-995-561-710	US-10-467-657-1642	US-10-821-234-1317	US-10-793-626-2448	US-10-858-730-12	US-10-858-730-13	US-10-858-730-208	US-10-793-626-218	US-10-793-626-804	US-10-793-626-648	US-10-467-657-1654	US-11-055-822-370	US-11-055-822-1002	US-11-055-822-368	US-11-055-822-1000
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	Ouery Match	61.1	61.1	6.09	6.09	60.8	59.8	58.3	57.6	57.6	57.4	54.7	22.9	22.0	21.5	19.7	19.5	18.7	17.6	17.5	16.8	6.1	5.7	5.7	5.7	5.7
	Score	1777.5	1777.5	1769.5	1769.5	1766.5	1739	1693.5	1673.5	1673.5	1669.5	1591.5	999	640.5	625	572	568	543.5	512.5	508.5	487	178	167	167	167	167
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Sequence 910, App Sequence 110, App Sequence 110, App Sequence 9, Appl Sequence 314, App Sequence 8056, Appl Sequence 116, App Sequence 5, Appli Sequence 6, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 16, Appli Se	3280
US-11-055-822-910 US-10-053-822-910 US-10-052-554A-9 US-11-143-980-50 US-11-143-980-50 US-10-793-626-3314 US-10-467-657-880-50 US-10-85-517-316 US-10-85-517-316 US-10-85-517-316 US-11-055-822-1146 US-11-166-609-18 US-11-166-609-18 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16 US-11-070-080-16	US-10-467-657-3280
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APPLICANT: Garrett-Engele, Philip W.
APPLICANT: Armoud, Christopher D.
APPLICANT: Raymond, Christopher D.
APPLICANT: Raymond, Christopher D.
APPLICANT: Castle, John C.
TITLE OF INVENTION: ALTERNATIVELY SPLICED ISOFORM OF TITLE OF INVENTION: ALTERNATIVELY SPLICED ISOFORM OF TITLE OF INVENTION ACETYL—COA CARBOXYLASE 2 (ACC2) FILE REFERENCE: RSO20
CURRENT APPLICATION NUMBER: 05/11/144,368
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: 60/577,234
PRIOR FILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FRASEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7;
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                                                                                                                    ; Sequence 4, Application US/11144368; Publication No. US20050272082A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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--VTPVSFETPLSPPIARGHVIAAR
                                                      242 ASP-AEFVTRFGGNRVIETVLIANNGIAAVKCMRSIRRWAYEMFRNERAIRFVVMVTPED
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TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2 SEQUENCES AND METHODS
FILLE REFERENCE: BMS DOCKET Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 16
LENGTH: 2455
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
ORGANISM: Rattus norvegicus
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PAAQLQIAMGVPLHRLKDIRLLYGESPWG-
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Best Local Similarity 63.4%
Matches 344; Conservative
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US-11-186-999-16
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Sequence 13, Application US/11186999
Publication No. US20060019364A1
GENERAL INFORMATION
TILLE OF INVENTION: ACETYL COA CARBOXYLASE 2 SEQUENCES AND METHODS
FILE REFERENCE: BND DOCKET Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VETSION 3.2
SOFTWARE: PATENTIN VETSION 3.2
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TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2 SEQUENCES AND METHODS
FILE REFERENCE: BMS Docket Number 10245 NP
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al Similarity 63.4%; Score 1769.5; DB 7; Length
al Similarity 63.4%; Pred. No. 1.1e-130;
344; Conservative 75; Mismatches 107; Indels
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                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-11-186-999-13
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Best Local Similarity
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                                                                                                                                         DB 7;
                                                                                                                                      60.8%; Score 1766.5; DB 7; 63.2%; Pred. No. 1.9e-130; ive 75; Mismatches 108;
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FILE REFERENCE: BMS DOCKET Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 2455
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 6
LENGTH: 2458
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Publication No. US20060019364A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
                                                                                                                                                   Best Local Similarity 63.2<sup>3</sup>
Matches 343; Conservative
                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-11-186-999-4
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ASP-AEFVTRXGGDRVIEKVLIANNGIAAVKCMRSIRRWAYEMFRNERAIRFVVMVTPED
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TITLE OF INVENTION: ACETYL COA CARBOXYLASE
FILLE REFERENCE: BMS DOCKET NUMBER 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
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US-11-186-999-8
Sequence 8, Application US/11186999
Publication No. US20060019364A1
GENERAL INFORMATION:
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TYPE: PRT
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Length 2455;
                              Indels
Query Match 59.8%; Score 1739; DB 7; Best Local Similarity 62.8%; Pred. No. 2.7e-128; Matches 341; Conservative 75; Mismatches 107;
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TITLE OF INVENTION ACETYL COA CARBOXTAGES:
FILE REPERBUCE: BMS DOCKET Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
WUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
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OTHER INFORMATION: Xaa is any amino acid
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Publication No. US20060019364A1
GENERAL INFORMATION:
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Matches 333; Conservative
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US-11-186-999-11
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LENGTH: 2458
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AVPEFMEQCAVILLAKTVVYVSAGTVGYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL
                                                                   PAAQLQVAMGIPLYSIRDIRTLYGNDPRGNEVIDFDFSSPESFKTQRKPQ-PQGHVVACR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/11186999
Publication No. US20060019364A1
GENERAL: INFORMATION:
APPLICANT: Briscol-Myers Squibb Company
TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2
FILE REFERENCE: BMS Docket Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Version 3.2
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Best Local Similarity 60.8%;
Matches 330; Conservative
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ORGANISM: Homo sapiens
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US-11-186-999-2
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TITLE OF INVENTION: ACETYL COA CARBOXYLASE
FILE REFERENCE: BMS Docket Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SCOTWARE: Patentin Version 3.2
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Publication No. US20060019364A1
GENERAL INFORMATION:
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; ORGANISM: Rattus norvegicus
US-11-186-999-10
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Matches 327; Conservative
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                                                                                                                                                         Sequence 710, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
FARELICANT: CARGILL, Michele et al.
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 710
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               AISNMVVALKELSLRGDFRTTVEYLINLLETESFQNNYIDTGWLDYLIAEKV-QKKPNIM 771
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ARKOMVISLKELSIRGDFRITVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPAD
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-995-561-710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 RIGYRGAGTFEFLY--EDGEFFFFIEMNTRVQVEHPVTELITGVDIVQEQLRIASGLPLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 SIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452 ALTELNFRSSTSTWGYFSVGTSGALHE-----YADSQFGHIFAYGADRSEARKQMVISL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86;
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                                                                                                        APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.9%; Score 666; DB 6; I
llarity 31.9%; Pred. No. 5.7e-45;
Conservative 92; Mismatches 180;
                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
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1 MLKKVLIANRGEIALRVLRACREMGIAT-
Sequence 1642, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:
APPLICANT: CHIRON SpA
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Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 1642
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US-10-467-657-1642
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168; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 AEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGS----PVFVMKLAGQAR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVG 335
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: P01348003
CURRENT APPLICATION NUMBER: US/10/793,626
PRIOR PILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Pacentin Ver: 2.1
LENGTH, 1151
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERENCE: 921A
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                     Length 703;
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                                                                                                                                                                                                                                                                               87; Mismatches 178;
                                                       CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: DC SEQ_Genes Version 1.0
SEQ ID NO 1317
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Publication No. US20050255478A1
GENERAL INFORMATION:
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                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: HOMO
US-10-821-234-1317
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Best Local Simi
Matches 166;
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158 AMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGL 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 ARHLEVQLLADQYGNAISIFGRDCSVQRRHQXIIEEAPVTIAPEDARESMEKAAVRLAKL 333
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                                                                                                                                                                                                                                                                                                                                                          98 VPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGS
                                                OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                          78;
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APPLICANT: Walbridge, Michael J.
APPLICANT: Vorgey, Peter S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: PRODUCTION
                                                                                                                                                  21.5%; Score 625; DB 6; Length 11
31.9%; Pred. No. 3.7e-41;
tive 91; Mismatches 182; Indels
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CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
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PRIOR FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: US 60/551,860
PRIOR FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
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ORGANISM: Artificial Sequence FEATURE:
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GENERAL INFORMATION:
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Madden, Kevin T.
                                                                                                                                                Query Match
Best Local Similarity 31.8*
Matches 164; Conservative
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O'Toole, George
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for Windows Version 4.0
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PRIOR FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
                                                                                                                                  Similarity
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 SOFTWARE: FastSEO
SEO ID NO 13
LENGTH: 1127
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                                                                                                               Query Match
Best Local S
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                                                                                                                                                                                                                                                                               54 QGHPVRAYLSVEBIVRAARRAGADAVYPGYGFLSENPEL--ARACEBAGITFVGPSARIL 111
                                                                                                                                                                                                                                                                                                               RSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEK 219
                                                                                                                                                                                                                                                                                                                                                112 ELTGNKARAVAAAREAGVPVL------GSSAPSTDV-----DELVRA 147
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                                                                                                                                                                               40 KVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVP 99
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                                                                                                                                                   Gaps
                                                                                                                                                 191
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APPLICANT: O'Toole, George
APPLICANT: O'Toole, George
APPLICANT: Trucheart, Joshua
APPLICANT: Trucheart, Joshua
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: 14184-030001
CURRENT APPLICATION NUMBER: US,10,858,730
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/475,000
PRIOR FILING DATE: 2004-03-10
PRIOR FILING DATE: 2004-03-10
                                                                                                               Length 1124;
                                                                                                                                                Indels
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                                                                                                               Query Match 19.7%; Score 572; DB 6; Lo
Best Local Similarity 30.8%; Pred. No. 5.3e-37;
Matches 161; Conservative 87; Mismatches 199;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/10858730 Publication No. US20050255568A1 GENERAL INFORMATION:
                                                                 ORGANISM: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blomquist, Paul
Doten, Reed
Driggers, Edward M.
Madden, Kevin T.
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50 ---QIGEV--GHPVRAYLSVDEIIRVAKHSGADAVYPGYGFLSENPDLAAKCAEA--GIT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTABEGLEKAEKIGYPVMIKASEGGGGGGIRKCTNGEEFKQLYNAVLGEVPG----SPVF 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 SSVDELMAAADMEFPLFVKAVSGGGGRGMRRVTDRESLAEAIEAASREAESAFGDASVY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 VMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : : ||:|||:||| || :: | |||||||||||||| IEQAVIAPRHIEVQILADGAGNVMHLFERDCSVQRRHQKVVBLAFAPNLSDELRQQICAD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 AVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI PAAQLQVAM 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 KPGMGALTELNFRSSTSTWGYFSVGTS-GA-LHEYADSQFGHIFAYGADRSEARKQMVIS 504
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                                                                                                                                                                                                                                                                                                                                 91 MADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKII
                                                                                                                                                                                                                                               FIGPPGSAMRSLGDXISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 GETLADL------GL------GL------SQDRLVVRGAAMOCKITTEVPANGF
                                                                                                                                                 Gaps
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APPLICANT: Doten, Reed
APPLICANT: Doten, Reed
APPLICANT: Doten, Reed
APPLICANT: Doten, Revard M.
APPLICANT: Doten, Kevin T.
APPLICANT: O'Leary, Jessica
APPLICANT: O'Toole, George
APPLICANT: Trueheart, Joshua
APPLICANT: Trueheart, Joshua
APPLICANT: Trueheart, Joshua
APPLICANT: Trueheart, Joshua
APPLICANT: Prorey, Peter S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: 14184-030001
CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2003-05-30
                                                                                     Length 1127;
                                                                                                                                                 Indels
                                                                                                                                                                                                            37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIBFTVMATPED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 568; DB 6; I; Pred. No. 1.1e-36; 88; Mismatches 196;
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, ORGANISM: Mycobacterium smegmatis US-10-858-730-13
                                                                                        19.5%;
30.5%;
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US-10-793-626-804
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                                                                                                                                                                                                                                 SAEGQTYPIFVKAVAGGGGRGMRFVASPDELRKLATEASREAEAAFGDGAVYVERAVINP 216
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                                                                                                                                                                                                                                                                                                                                KAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGS----PVFVMKLAGQA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                GYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454
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                                                                                                                                                                                   14 KILVANRGEIAVRAFRA----ALETGA-----ATVAIYPREDR-GSFHRSFASEAVRIG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PALENTIN VET. 2.1
                                                                                                                                                                                                                                                                        MRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLE
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                                                                                                                                Gaps
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                                                                                                                             Indels 101;
                                                                                                    Length 1140
                                                                                                 DB 6;
                                                                                                                             90; Mismatches 188;
                                                                                                               .5e-35
                                                                                               18.7%; Score 543.5; 29.3%; Pred. No. 9.5
  for Windows Version 4.0
                                                     ORGANISM: Coryne-bacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 218, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
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                                                                                                                        Matches 157; Conservative
                                                                                                              Similarity
SOFTWARE: FABLSEQ f
SEQ ID NO 208
LENGTH: 1140
TYPE: PRT
                                                                   US-10-858-730-208
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LENGTH: 341
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Best Local
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Score 512.5; DB 6; Length 341; Pred. No. 4.5e-33;

17.6**%**; 31.7**%**;

Query Match Best Local Similarity

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GEFAFLELNPRLOVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVI 410
                                                                                                                                                                                                                                                                                                                                                                                                                    ----EAL 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 G------TSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVE 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 AICIGEANPLDSYLNIDRIISAAKVTESNVIHPGYGFLSESTNFAK--AVEDNHIHFIGP 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 804, Application US/10793626
Publication No. US20050255478a1
GENERAL INPORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
                                                                                              -- BGLİQSIDDAKKIAKKİGYPVIIKATAG
                                              175 ADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEG
                                                                                                                                                                                                                                                      291 SIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPES
                                                                                                                                                  235 GGGKGIRKCTNGEEFKQLYNAVLGEVP----GSPVFVMKLAGQARHLEVQLLADQYGNAI
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PRIOR APPLICATION WINBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
  61,
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ORGANISM: Artificial Sequence
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Conservative
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                                                                                                 14 ANVPVVPGS--
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OY 471 GISGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRITTT	Qy 520 YLIKLLET 527   : ::    Db 299 YLVLGIDT 306	RESULT 21 US-10-467-657-1654 ; Sequence 1654, Application US/10467657 ; Publication No. US20050260581A1	; GENERAL INFORMATION: ; APPLICANT: CHIRON SpA ; APPLICANT: FONTANA MARIA Rita . ADDITCANT: DIZZA MARIARIA RITA	APPLICANT: MASIGNANT VEGA APPLICANT: MONACI Blisabetta TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS FILE REFERENCE:	CURRENT APPLICATION NUMBER: US/10/467,657  CURRENT FILING DATE: 2003-08-11  PRIOR APPLICATION NUMBER: GB-0103424.8  PRIOR FILING DATE: 2001-02-12  NUMBER OF SEQ. ID NOS: 9218  SOFTWARE: Sequingly, version 1.04	1654 1071 RT M: Neisseria 57-1654	Query Match 6.1%; Score 178; DB 6; Length 1071; Best Local Similarity 21.8%; Pred. No. 4.9e-06; Matches 79; Conservative 66; Mismatches 162; Indels 56; Gapi	OY 211 HTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVF'	Qy 269 KLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEA-PVTIAPEDAR :	OY 323 MEKAAVRLAKLVGYVSAGT-VEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI PA	Qy 382 LQVAMGIPLYSIR-DIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVAC :	Qy 438 TAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRS	Qy 498 RKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAE 	Qy 554 PAD 556  Db 471 VSD 473	RESULT 22 US-11-055-822-370 Command 370 April 2011 OF E022	Publication No. US20050260707A1 GENERAL INFORMATION: APPLICANT: Pompejus, Markus APPLICANT: Kroger, Burkhard
271 AGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRL  :-	DD 203 IPVAKHVEVQIIGDGKNNYVHLGERDCSVQRKNQKLIEEAPCAALTEERRTRICGDAVKV 262 QY 331 AKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPL 390	391 YSIRDIRTLYGMDFRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITABNPDTGFKPGM :	<pre>Qy</pre>	OY 505 LKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLD 541	RESULT 20 US-10-793-626-648 ; Sequence 648, Application US/10793626 ; Publication No. US20050255478A1 ; GENERAL INFORMATION:	APPLICANT: KIMMERLY, WILLIAM JOHN TITLE OF INVENTION: STAPHYLCCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS FILE REFERENCE: PU3480US CURRENT APPLICATION NUMBER: US/10/793,626 CURRENT FILING DATE: 2004-03-04	FRIOR APPLICATION NUMBER: 60/164,258 PRIOR FILING DATE: 1999-11-09 NUMBER OF SEQ ID NOS: 4472 SOFTWARE: Patentin Ver. 2.1	SEQ IN NO 948 I ENGTH: 309 TYPE: PRT ORGANISM: Artificial Sequence	FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence FEATURE: NAME (FEATURE: NAME (FEATURE)	NATIONALON: (1905) I DOCHION: (1907) OTHER INFORMATION: variable amino acid US-10-793-626-648	Query Match Best Local Similarity 31.8%; Pred. No. 3.9e-31; Matches 117; Conservative 53; Mismatches 108; Indels 90; Gaps 7;	Qy     175 ADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEG 234	Qy 235 GGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGOARHLEVQLLADQYGNAI 290	QY 291 SIFGRDCSVQRRHQKIIERAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPES 350 	QY         351 GEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLGVAMGIPLYSIRDIRTLYGMDPRGNEVI 410           :	Qy 411 DFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPCMGALTELNFRSSTSTWGYFSV 470

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Saps 15;
PVFVM 268
PLLIE 207
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|::|
OKAEI 419
JARES 322
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CEYQI 263
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CEEKS 470
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RESULT 23
US-11-055-822-1002
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Sequence 1002, Application US/11055822 Publication No. US20050260707A1

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CURRENT FILING DATE: 2005-02-11

PRIOR FAPLICATION NUMBER: US/11/055,822

CURRENT FILING DATE: 2000-06-23

PRIOR FILING DATE: 1999-06-25

PRIOR FILING DATE: 1999-07-02

PRIOR FILING DATE: 1999-07-02

PRIOR FILING DATE: 1999-08-12

PRIOR FILING DATE: 1999-08-12

PRIOR FILING DATE: 1999-08-12

PRIOR FILING DATE: 1999-08-12

PRIOR FILING DATE: 1999-08-12

PRIOR FILING DATE: 1999-08-12

PRIOR FILING DATE: 1999-07-0

PRIOR FILING DATE: 1999-07-0

PRIOR FILING DATE: 1999-07-0

PRIOR PAPLICATION NUMBER: DE 19931418.7

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: DE 19931419.5

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-08 i TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
US-11-055-822-370 264 718 312 168 셤 셤 셤 d ò ઠે ò ò 유

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                                                                            CTERIUM GLUTAMICUM GENES ENCODING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 167; DB 7; 22.2%; Pred. No. 3.5e-05;
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
IITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM (
ITITE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1939-06-25
PRIOR FILING DATE: 1939-07-02
PRIOR PELING DATE: 1939-07-02
PRIOR FILING DATE: 1939-07-02
PRIOR FILING DATE: 1939-08-12
PRIOR PELICATION NUMBER: 60/187,970
PRIOR PILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 1930476.9
PRIOR FILING DATE: 1939-07-01
PRIOR FILING DATE: 1939-07-08
PRIOR FILING DATE: 1939-07-08
PRIOR PLICATION NUMBER: DE 1931415.2
PRIOR PLICATION NUMBER: DE 1931416.7
PRIOR PLILING DATE: 1939-07-08
PRIOR PLILING DATE: 1939-07-08
PRIOR PLILING DATE: 1939-07-08
                                                                                                                                                      CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
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PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 1002
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PRIOR APPLICATION NUMBER: 60/141,031
                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-06-25
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Matches 92; Conservative
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) ORGANISM: Corynebacterium glutamicum
US-11-055-822-1000
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APPLICANT: Schroder, Harrwig
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
TITLE OF INVENTION: CRYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
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                                                                                                                                   THILE REFERENCE AGG - LANGER BOLLO FATHWAY PROJEST CURRENT APPLICATION NUMBER: US/11/055,822 CURRENT APPLICATION NUMBER: US/11/055,822 CURRENT APPLICATION NUMBER: 09/606,740 PRIOR FILING DATE: 2000-06-23 PRIOR PELING DATE: 1999-06-25 PRIOR PELING DATE: 1999-06-25 PRIOR APPLICATION NUMBER: 60/141,031 PRIOR PILING DATE: 1999-07-02 PRIOR PILING DATE: 1999-07-02 PRIOR PELING DATE: 1999-07-02 PRIOR PILING DATE: 1999-07-03 PRIOR PILING DATE: 1999-07-09 PRIOR PILING DATE: 1999-07-09 PRIOR PILING DATE: 1999-07-01 PRIOR PILING DATE: 1999-07-01 PRIOR APPLICATION NUMBER: DE 19931415.2 PRIOR APPLICATION NUMBER: DE 19931418.7 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08 PRIOR PILING DATE: 1999-07-08
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VFVTVANRD--KRTLILPIQRLALMG-
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US-11-055-822-368
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Best Local S
Matches 92
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372 VSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKP---- 426
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SEQ ID NO 1000
LENGTH: 1113
APPLICANT: Pompel us, Markhads
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Oskar
APPLICANT: Schroder, Oskar
APPLICANT: APPLICANT: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: ORNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE OF INVENTION: MUMBER: US/11/055,822
CURRENT APPLICATION NUMBER: 09/606,740
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR PELING DATE: 1999-06-25
PRIOR PELING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR PELING DATE: 1999-07-02
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PRIOR PELING DATE: 1999-07-03
PRIOR PELING DATE: 1999-07-04
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218 EQGINAREIEVAVLGNDY 235
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ORGANISM: Artificial Sequence
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US-10-793-626-3294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 EGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL--GEVPGSPVFV---MK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 LAGGARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEE-APVTIAPEDARESMEKAAV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 FDYEITLLTVRSIDPTTSKPATWPCEPIGHROEDGDYVESWOPMEMTPR-ALENARSVAA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKVMLLGSG------VDRYEHA 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 RLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPT-----TEMVSGVNIPA-AQ 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ::::| :::| S1 PA----HQVAHFSYVIDMIDAAQVREL-----VERVRPDFVIPEIEALATDELVKIEE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVWATPEDLKVNADYIRMADQYVEV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 EGLA-----TIVPT-ARAAKLTMNREGIRKLAAEELGLPTSN----YEFC-STFE
                        487 IFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - See File Wrapper or PALM
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                                                                                                                                                                                                                                                                       APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REPERBYCE: BG1-1212PCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT APPLICATION NUMBER: 09/66,740
PRIOR APPLICATION NUMBER: 09/66,740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.8%; Score 110; DB 7; Length 408; Best Local Similarity 21.6%; Pred. No. 0.27; Matches 90; Conservative 66; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR PELICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR PELICATION NUMBER: 60/187,970
PRIOR PELING DATE: 2000-03-09
PRIOR PELING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR PILING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931416.7
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
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NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 910
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                                                                                                                                                     Sequence 910, Application US/11055822
Publication No. US20050260707A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-055-822-910,
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ORGANISM:
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Sequence 1010, Application US/10453372

Sequence 1010, Application US/10453372

Publication No. US20060003323A1

GENERAL INPORMATION:

APPLICANT: Alsobrook, et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH

FILE REPERENCE: 21402-589 A

CURRENT PAPLICATION NUMBER: 09/789390

PRIOR APPLICATION NUMBER: 09/789390

PRIOR APPLICATION NUMBER: 09/789390

PRIOR APPLICATION NUMBER: 09/189390

PRIOR PILING DATE: 2000-03-01

PRIOR PILING DATE: 2000-03-01

PRIOR PILING DATE: 2000-03-10

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-03-19

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-03-23

PRIOR PILING DATE: 2001-03-23

PRIOR PILING DATE: 2001-05-23

PRIOR PILING DATE: 2001-05-23

PRIOR PILING DATE: 2001-05-23
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263 RITNALGGRGVFGVELFVSGD--DVYFSEVSPR---PHDTGLVTLATQRFSEFELHAKAI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 IPYVGNGVLAASSSMDKLVMKQLFEHRGLPQLPYI-----SPLRSEYEKYENN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 CIHTABEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEBFKQLYNAVLGEVPGSPVFVM 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 IİXLVN-----DKLTYPVFVKPANLGSSVGISKCNNEBELK---SGIAEAFQFDRKLVI 217
                                                                                                                                                                                                                                                                         Publication No. US2005025478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PUBLICATION NUMBER:
CURRENT FILING DATE: 2004-03-04
PRIOR PAPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Batentin Ver. 2.1
LENGTH: 271
                                                                                 382 LQVAMGIPLYSIRDIRTLY-GMDPRGNE------VIDFD---FSSPESFKTQR 424
                                                                                                                           149 IIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic;
OTHER INFORMATION: amino acid sequence
US-10-793-626-3294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 101.5; D
Best Local Similarity 24.6%; Pred. No. 1.1;
Matches 34; Conservative 21; Mismatches
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TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex TITLE OF INVENTION: Polyketide FILE REFERENCE: AM-101426US CURRENT APPLICATION NUMBER: US/11/143,980 CURRENT FILING DATE: 2005-06-03 PRIOR APPLICATION NUMBER: US 60/664,483
                                                                                                                                                                                                                                                                                                                                             ----TAYTDNNGYAYVNLL 1046
                                                                                                                                                                                                                                                                                                                                                                                                                    965 DNKTFS-----LSVLPDESSAKVISITGAEKTITVGENITLRILVODAFNNVIAGORV 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1221 TKGSPVVNIPTTRTDQSGQVTATITSTLAETLTVNVQVPGTANQSATITLVAGTADESKS 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 RESMEKAAVRLAKL.--VGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ITAENPDTGFKPGMGALTELNFRSS-----TSTWGYFSVGTSGALHEYADSQFGH 486
                                                                                                                                                                                                                                                                                                                                                                                       114 VDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQ
                                                                                                                                                                                                                                                                                               54 IRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------EGLEKA------EKIGYPVM-IKASEGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1281 ILKSDVDTLKADYQQSAKLTLTLQDKYGNPI-----VTSDHLEFVQSGPF-----
                                                                                                                                                                                                          4 DHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVIT-----KVLI----CNNGIAAVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 HADVPCMP-----WSGTGIKETMMSDQGFLTVSDD---VYQQACI----
                                                                                                                                                             247;
                                                                                                                    Length 1579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1393 TFSTAKFPSEGFAGAYYTLNNDNFEAGKTVDDYMFSSSQGWVSVDASGKVS-
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKG-----IRKCTNGEEPKQLYN-----AVLGEVPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487 IFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKL 524
                                                                                                                                                             68; Mismatches 198;
                                                                                                                    DB 7;
                                                                                                                                                                                                                                                                                                                                        1018 RLSAQPITNITIGD------
                                                                                                                  3.4%; Score 98.5; 19.6%; Pred. No. 15;
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                          ) TYPE: PRT
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wagenaar, Melissa
Graziani, Edmund
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Kulowski, Kerry
                                                                                                                                                               Conservative
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APPLICANT: Hucul, John
APPLICANT: Haltli, Brad
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                                                                                                               Query Match
Best Local Similarity
Matches 125; Conserv
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    LENGTH: 1579
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                    27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGDKISSTIV--AQHADVPCMPWSG-----TGIK-----ETWMSDQG----FL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 INEGLPAGVLIGSLAEDLRLLFRSAGRPDPQSQLPERTGAEWNPPLSFSLASRGLSGQYV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TAWSG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EV-----PGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 IAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 VGTSGALHEYADSQFGH----IFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLL 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---FHLDENTGVIKLFSKI 382
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3.4%; Score 98.5; DB 6; Length 947;
Best Local Similarity 19.1%; Pred. No. 7.3;
Matches 94; Conservative 70; Mismatches 144; Indels 183;
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Sequence 9, Application US/11052554A

Publication No. US2005028866A1

GENERAL INFORMATION:

APPLICANT: Sachdeva, et al.

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDER

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTT

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTT

TITLE OF INVENTION: WIMBER: US 60/589,257

PRIOR FILING DATE: 2004-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

NUMBER OF SEQ ID NOS: 763

SEQ ID NO 9
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - 8
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO: 1000
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                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
US-10-453-372-1010
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us-10-633-835-2; rapbn

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APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 SSTIVAQHA-----
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 20.29
Matches 70; Conservative
                                                                                                                                                                     284 DQY 286
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Sequence 314, Application US/10793626

Publication No. US2005025478A1

GENERAL INPORMATION:
TITLE OF INVENTION: TAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

TITLE OF INVENTION: TAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT PILING DATE: 2004-03-04

PRIOR FILING DATE: 1999-1109

NUMBER: OF SEQ ID NOS: 4472

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 3314
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                                                                                                                                                                                                                                                                                                                                                                                   101 GSNNNNYANVDLIVDVAE-----RAGVHAV------WAGWGHASENPRLPESLA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 ASKHKIIFIGPPGSAMRSL---GDKISSTIVAQHADV---PCMPWSGTGIKETMMSDQGF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNAVLGEVPGSPVFVMKLAG--QARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEA 310
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                                                                                                                                                                                                                                                3 PDHKAVSQFIGGNPLETAP---ASPVA---DFIRKQGGHSVITKVLICNNGIA---AVKE
                                                                                                                                                                                                                                                                                                                 54 IRSIRKW-AYETFGDERAIEFT--VMATP----BDLKVNADYIRMADQYVEVPG-
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OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                   Length 3073;
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Pred. No. 1.3;
                                                                                                                                                              Query Match 3.4%; Score 97.5; UD '' Best Local Similarity 21.7%; Pred. No. 48; Conservative 57; Mismatches 194; Indels
                   60/576,895
PRIOR FILING DATE: 2005-03-23
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2004-06-03
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 50
LENGTH: 3073
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                                                                                                              ; TYPE: PRT
; ORGANISM: Streptomyces sp.
US-11-143-980-50
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Best Local Similarity
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                                                 DKISSTIVAQHADVPCMPWSGTGIKETWMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKI
                                                                                                                                                   224 GYPVMIKASEGGGGKGIRKCTNGEEFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLA
                                                                                                    ---SFLRSEYEKYENNIIKLVN-----DKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 HKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
  53;
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Mismatches
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CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 8056
LENGTH: 717
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8056, Application US/10467657
Publication No. US20050260581A1
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                                                                                               2 DKLVMKQLFEHRGLPQLPYI----
19;
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us-10-633-835-2.rapbn

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Sequence 5, Application US/10519531 Publication No. US20050244429A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 DKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLA 283
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19.3%; Pred. No. 4.7;
tive 55; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                     Length 393
                                                                                                                                                                                                                                                                                                                                                                                                          71; Indels
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Sequence 4, Application US/10519531

Publication No. US2005024429A1

GENERAL INFORMATION: TO THE OF INVERTION: LIVE REPLICATION:

TITLE OF INVERTION: LIVE REPLICATION SPUMAVIRUS VECTOR

FILE REFERENCE: 14114.0373U2

CURRENT FILING DATE: 2004-12-27

PRIOR APPLICATION NUMBER: US/10/519,531

PRIOR FILING DATE: 2003-06-27

PRIOR APPLICATION NUMBER: 60/392,630

PRIOR APPLICATION NUMBER: 60/392,630
                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                            APPLICANT: Foster, Simon APPLICANT: Foster, Simon APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P10062940
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2002-01-09
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SEQ ID NO 316
                                                                                                                                                                                                                                                                                                                                                                     Query Match
3.3%; Score 96; DB (Best Local Similarity 22.6%; Pred. No. 3.2; Matches 42; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            130 GHASE-NPRLPESLAASKHKIIF---IGPPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 512
                     Biosynexus Incorporated
University of Sheffield
                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-316
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Matches 88; Conservative
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NDYPEA 270
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APPLICANT:
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151 FIGPPGSAM------RSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTV 200
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                                                                                                                                                                                                                                                                                                                                                                           201 SDDVYQQACIHTABEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEV 260
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                                 215 VHPVHAGPIAPGQMREPRGSDIAGTISTLQEQIGWMINNPPIPVGEIYKRWIILGLNKIV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                       331 KTILKALGPAATLEE-----375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 VHPVHAGPIAPGOMREPRGSDIAGTTSTLOEQIGWMTNNPPIPVGEIYKRWIILGLNKIV 274
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70 AIEFTVM----ATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLI-----VDVAERAG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IMMORGNFRNORKIVKCFNCGKEGHI-ARNCRAPRKKGCWKCGKEGHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FOLKE, Thomas M.
TITLE OF INVENTION: LIVE REPLICATING SPUMAVIRUS VECTOR
FILE REFERENCE: 14114.037342
CURRENT APPLICATION NUMBER: US/10/519,531
CURRENT FILING DATE: 2004-12-27
FRIOR APPLICATION NUMBER: PCT/US03/20325
PRIOR FILING DATE: 2003-06-27
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 8
SOFTWARRE: FASESEQ for Windows Version 4.0
SEQ ID NO 5
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TLITPEQQVLKAAIIYSSPYTPMLFMGEEFGATTPFAFFCSHTDPELNRLTSEGRKREFA 490
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                                                                           DVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKG
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                                   ENPRIPESIAASKHKIIFIGPPG---SAMRSLGDKISSTIVAQHADVPCMPWSGTG----
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20.9%; Pred. No. 6;
tive 59; Mismatches 188; Indels 140;
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PRIOR FILING DATE: 2002-11-18
PRIOR FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 60/316,276
PRIOR APPLICATION NUMBER: DE 101 39 062.9
PRIOR APPLICATION NUMBER: DE 101 39 062.9
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 610
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APPLICANT: HERWANN, THOMAS
APPLICANT: HERWANN, THOMAS
APPLICANT: MCRACH, SUSANNE
APPLICANT: RALEMER, REINHARD
TITLE OF INVENTION: PROCESS FOR THE FERMENT;
TITLE OF INVENTION: CORYNEFORM BACTERIA
FILE REFREENCE: 223168USOR
CURRENT APPLICATION NUMBER: US/11/124,291
CURRENT FILING DATE: 2005-09
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Publication No. US20050266536A1
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Best Local Similarity 20.99
Matches 102; Conservative
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275 RMYSPTSILDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNW----MTETLLVQNANPDC 330
                                                    SDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEV 260
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20.9%; Pred. No. 6;
tive 59; Mismatches 188; Indels 140;
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                                                                                                                                                                261 PGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRR-
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APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORVNEBACTERIUM GLUTAMICUM G
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
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PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 1993446.9
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR PRILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR PRILING DATE: 1999-07-08
PRIOR PRILING DATE: 1999-07-08
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CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1146, Application US/11055822 Publication No. US20050260707A1 GENERAL INFORMATION:
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                                                                                                            331 KTILKALGPAATLEE-
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Best Local Similarity 20.99
Matches 102; Conservative
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Qy. 192	Db 236 LWRLKKFLHVGSBALLEGSMKLVDDFTYSVIRRRKABILQARASGKQEKIKHDILSRFIE 295	Qy 231 ASEGGGKGIRKCTNGEEFKQLYNAVLGEVPGS	Db 296 LGEAGGDEGGGSFGDDKSLRDVVLNFVIAGRDTTATTLSWFTYMAMTHPAVADK 349	QY 270 LAGGARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVT 313	DD 350 LRRELAAFEDERAREGVALADAAGEASFAARVAQFASLLSYDAVGKLVYLHACVTETLR 409	Qy 314IAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEF 353	Db 410 LYPAVPQDPKGIVEDDVLPDGTKVRAGGMVTYVPYSMGRMEYNWGPDAASFRPERWLSGD 469	OY 354AFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPL 390	Db 470 GGAFRNASPFKFTAFQAGPRICLGKDSAYLQMKWALAI 507	or Titioad	NSJUL 33 US-11-554A-8 : Sequence 8. Application US/11052554A	; Publication No. US20050288866A1 ; GENERAL INFORMATION:	COMPUTATIONAL METHOD FOR	PROTEINS OF	CURRENT APPLICATION NUMBER: US/11/052,554A  CURRENT FILING DATE: 2005-02-07	NUMBER: US : 2004-07-20	; PRIOR APPLICATION NUMBER: IN 173/DEL/2004 ; PRIOR FILING DATE: 2004-02-06	NUMBER OF SEQ ID NOS: 763	8 1417	TYPE: PHOREANISM		3.3%; Score 95.5; DB 7; Length 1417; lmilarity 23.5%; Pred. No. 22;	Matches 64; Conservative 23; Mismatches 120; Indels 65; Gaps	OY 231 ABEGGGGGKIRKTINGEEFKOLYNAVLGEVPGSPVFVMKLAGQAKHLEVQLLANDOYG 28/   :	288 NAISIEGRDCSVORRHOXIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWL		Qy 346 YSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSI 393	Db 843TEKGNGSYVATLTTGGKTGELRVMPLFNGQPAATEAAQLTVIAG-EMSSA 891	Qy 394 RDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPG 449	DD 892 NSTLVADNKAPTVKTTTELTFTVKDAYGNPVTGLKPDAPVF 932	Qy 450 MGALTELNPRSSTSTWGYPSVGTSGA 475	Db 933 SGAASTGSERPSAGNWTEKGNGVYVSTLTLGS 964	RESULT 40 11S-11-070-080-16	; Sequence 16, Application US/11070080 ; Publication No. US20050287625A1
Db 260 DEVR-NYILDAARQWFEDFHVDGLRLDAVHSLDDRGAYSLLAQLTMVAEDVSAQTGIPRS 318	Cy 187 - IKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKG 239	Db 319 LIAESELNDPKFVTSREAGGFGLDAQWVDDIHHALHALVSGERNGYYSDFGSVDT 373	QY 240 IRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDC 297	Db 374 LAK-TLREVFEHTGNYSTYRGRNHGRPVH-PDITPASRFVTYTTTHDQTGNR-AIGDRPS 430	Oy 298 SVORRHOKIIEEAPVTIAPEDA 319	: : :	Qy 320 RESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEM 371	Db 491 RLGWNADDIPSPELESTFTSSKLDWEFTAEQRRINDAYKQLLHLRHTLGFSQPNLLTLEV 550	DFD.	Db 551 EHGENWLSMANGRGRILANFSDDTITVPLGGELI-YSFTSPTVTDTSTTLQ 600	Qy 428 PQGHVVACR 436	Db 601 PMGPAILTR 609	RESULT 38	US-11-166-609-18 ; Sequence 18, Application US/11166609	; Publication No. US20060015968A1 ; GENERAL INFORMATION:	~	; APPLICANT: HUFFMAN, GARY ; APPLICANT: TRIMNELL, MARY	NVENTION: N	; FILE REFERENCE: 1148CR ; CURRENT APPLICATION NUMBER: US/11/166,609	; CURRENT FILING DATE: 2005-06-24 ; PRIOR APPLICATION NUMBER: 10/412,000	; PRIOR FILING DATE: 2003-04-11 ; PRIOR APPLICATION NUMBER: 09/670,153	SEQ ID NOS: 34	; SOFTWARE: Patentin Ver. 3.3 ; SEQ ID NO 18	; LENGTH: 544 ; TYPE: PRT : ORGANISM: Orvza sativa	-18	atch 3.3%; Score 95.5; DB 7; Length 544; cal Similarity 19.7%; Pred. No. 5.6;	Matches 103; Conservative 63; Mismatches 192; Indels 165; Gaps	Qy 15 NPLETAPASSVADFIRKQGGHSVITKYLICNNGIAAVKEI 54  1 -  - - - - - - - - - - - - - - - - -	S SETULNICATION TO THE TANGETT DAY BOTTON TO THE TANGETT DAY BOTTON TO THE TANGETT DAY BY THE TOP TO THE TANGETT DEPOSITION TO THE TANGET DEPOSITION TO THE TANGET DEPOSITION TO THE TANGET DEPOSITION TO THE TANGET DEPOSITION TO THE TANGET DEPOSITION TO THE TANGETT DEPOSITION TO THE TANGET DEPOSITION TO THE TANGET DEPOSITION TO TH	63 KNYHRMHDMIVEXLEKDRIVYTVDMPFTSYTYIADPVNVEHV-LKTNFTNYPKGEVY	איסטרים אינו די עונעם אינים אי	UY 100 NNIANY NILONO TO TO THE TOTAL OF THE	Qy 159 MRSLGDKISSTIVAQHADVPCMPWSGTGIKETM 191	DD 176 CKAGRVVDMQELFMRWTLDSİCKVGFGVEİGTLSPDLPENSFAQAFDAANİİVTLRFIDP 235

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100 GGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAM 159
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3.3%; Score 95; DB 7; Length 423;
Best Local Similarity 21.1%; Pred. No. 4.2;
Matches 66; Conservative 57; Mismatches 124; Indels
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Job time : 20 secs
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; ORGANISM: Methylomonas sp. 16a
US-11-070-080-16
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. Copyright

OM protein - protein search, using sw model

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4, 2006, 18:05:02 ; Search time 203 Seconds (without alignments) 1209.915 Million cell updates/sec

2907 1 PPPDHKAVSQFIGGNPLETA.....LDGLIQDRLTAERPPADLAV 559 US-10-633-835-2 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

2443163 seqs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

.2443163

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s: geneseqp2005s:\* A Geneseq Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Leng	88	ID	Description
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7	2222	76.4	2214	8	ADN10916	Pha
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9	2079.5	71.5	2241	æ	ADN19477	_
7	2061.5	70.9	2270	~	AAY24150	_
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14	1889.5	65.0	2000	7	ADK63986	∵
15	1790	61.6	632	œ	ADJ47655	_
16	1787	61.5	2346	œ	ADQ90744	Human
17.	1781	61.3	2346	ø	ABP70270	Abp70270 Amino aci
18	1781	61.3	2346	9	ABP59197	Human
19	1781	61.3	2346	9	ABP59195	Abp59195 Human ace
20	1781		2346	9	ABP59198	Abp59198 Human ace
21	1780	61.2	2348	4	ABB59490	Abb59490 Drosophil
22	1780		2348	ß	AA019075	Aao19075 Drosophil
23	1780	61.2	2348	Ŋ	ABB83866	Abb83866 Drosophil
24	1775	61.1	2288	4	AAB86033	_

Aar05707 Acetvl-Co	Abm83569 Human dia	Human	Abb84649 Human SEC	Abu65149 Human NOV	Human	Adj47656 Human ACC	Antips	Adq90746 Human ace	Adq39507 Human myo			Add39504 Human myo		Aar67819 Acetyl Co	Abb91251 Herbicida	Aaq50615 Arabidops	•	9 ACCas	Aay22129 Arabidops	-
AAR05707	ABM83569	ABP59211	ABB84649	ABU65149	ADN61949	ADJ47656	ADN03634	ADQ90746	ADQ39507	AEA33628	ADJ47652	ADQ39504	AAU32848	AAR67819	ABB91251	AAG50615	ADN72177	AAR76949	AAY22129	AAY40598
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61.0	6.09	6.09	6.09	60.9	60.4	59.8	58.4	. 57.4	57.4	57.4	55.2	54.7	54.7	54.5	54.4	54.3	54.3	54.3	54.3	54.3
1774	1769.5	1769.5	1769.5	1769.5	1756.5	1738	1697.5	1669.5	1669.5	1669.5	1604	1591.5	1591.5	1583	1581.5	1579	1579	1579	1578	1578
25	56	27	28	29	30	31	32	33	34	32	36	37	38	. 39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 ADJ47651

ADJ47651 standard; protein; 559 AA

ADJ47651;

(first entry) 06-MAY-2004

U. maydis ACCase BC domain SEQ ID NO:2.

ACCase; Acetyl CoA carboxylase; carboxy transferase domain; biotin carboxylase domain; BC domain; fungicide.

Ustilago maydis.

WO2004013159-A2.

12-FEB-2004.

04-AUG-2003; 2003WO-US024356.

05-AUG-2002; 2002US-0401170P.

(CROP-) CROPSOLUTION INC.

Weatherly SC; Volrath SL, Elich TD,

WPI; 2004-180421/17.

Novel peptide comprising acetyl COA carboxylase (ACCase) having deleted biotin binding domain and carboxy transferase domain, and having functional biotin carboxylase domain, useful for identifying ACCase inhibitors/activators. Novel

Claim 8; SEQ ID NO 2; 56pp; English

The invention relates to a novel peptide (I) comprising an acetyl CoA carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxy transferase domain, and having a functional biotin carboxylase domain. A peptide of the invention is useful for identifying Acetyl CoA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding compound in 

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activity, and selecting a compound that inhibits or activates Acetyl Coacarboxylase activity. A peptide of the invention is also useful for identifying fungicides, which involves combining the peptide and a compound to be tested for the ability to bind to the bictin carboxylase domain, under conditions that permit binding to the bictin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase arboxylase domain, the presence of binding indicating the compound is or may be fungicide, employing the identified compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound that inhibits Acetyl CoA carboxylase activity, The present sequence represents an ACCase BC domain of the invention.
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inhibition or
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Sequence 559 AA;

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  Length 559;
Score 2874; DB 8; Length 5
Pred. No. 5.2e-261;
1; Mismatches 5; Indels
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Query Match
Best Local Similarity 98.9%;
Matches 553; Conservative
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standard; protein; 2214 AA. ADN10916 RESULT

(first entry 01-JUL-2004 ADN10916

Phaffia rhodozyma acetyl-CoA carboxylase

antioxidant Acetyl-CoA carboxylase; enzyme; astaxanthin; pigment;

Xanthophyllomyces dendrorhous.

364

The present sequence is the protein sequence of the acetyl-CoA carboxylase (ACC) gene of Phaffia rhodozyma (ATCC 74438). The sequence shows 56.284 mainto acid sequence identity to a known ACC from Emericella nidulans. ACC is an enzyme involved in fatty acid biosynthesis. Its substrate is acetyl-CoA, which is also involved in the carotenogenic pathway of P. rhodozyma. A claimed method for producing ACC comprises culturing a recombinant organism containing a vector comprising an ACC polynucleotide. Also claimed is a resombinant organism in which gene expression of ACC is reduced as a result of antisense technology, site-directed mutagenesis, error-prone PCR or dentical mutagenesis. The recombinant organism is preferably P. rhodozyma or Xanthoppylomyces dendirorhous containing a vector comprising an antisense polynucleotide. It is used in a claimed process for producing carotenoids such as astaxanthin, beta-carotene, lycopene, zeaxanthin and canthaxanthin. The method is useful for increasing microbial production of carotenoids such as a staxanthin, which has antioxidant properties and is used as a second as a setaxanthin, which has antioxidant properties and is used as a New acetyl-CoA carboxylase polynucleotide derived from Phaffia rhodozyma or Xanthophylomyces dendrorhous, useful for producing a recombinant vector or for increasing microbial production of carotenoids. Claim 1; SEQ ID NO 3; 82pp; English × Setoguchi 25-SEP-2003; 2003WO-EP010683 27-SEP-2002; 2002EP-00021625 WPI; 2004-329883/30. N-PSDB; ADN10914, ADN10915. (STAM ) DSM IP ASSETS Ojima K, WO2004029232-A2 Hoshino T, 08-APR-2004 

Sequence 2214 AA;

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Gaps

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Length 2214; Indels

183 123 64 TFGDERAIEFTVMATPEDLKVNCDYIRMADRVVEVPGGTNNNNHSNVDLIVDIAERFNIH 123 GTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKC 243 244 INGEEFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRH 303 303 304 QKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQ 363 363 423 63 63 304 QKIIEEAPVTIARPERFEEMEKAAVRLAKLVGYVSAGTVEYLYSHADDSFFFLELNPRLQ 4 DHESVRHPIGGNALENAPPSSVTDFVRSQDGHTVITKVLIANNGIAAVKEIRSVRKWAYE VEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQ 4 DHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYE 64 TFGDERALEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVH 124 AVWAGWGHASENPRLPESLAASKGKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWS 76.4%; Score 2222; DB 8; 76.3%; Pred. No. 1.4e-198; ive 49; Mismatches 83; Query Match 76.4° Best Local Similarity 76.3° Matches 424; Conservative 184 364

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483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the deduced amino acid sequence of acetyl coenzyme A carboxylase (ACoACase, BC.6.4.1.2) from powdery mildew (Erysiphe graminis f.sp. hordei 23DS). It was deduced from a 8123 bp DNA sequence isolated from an ECARI genomic library by screening with a fragment of the Saccharomyces cerevisiae ACoACase gene. The amino acid aguence has 63 % identity and 77 % similarity to the yeast enzyme; it also has 47 % identity (ACA % similarity) with the ACOACase proteins from rat and chicken. ACOACase activity is the preferred target biochemical activity in a new screening system. (Updated on 16-OCT-2003 to
                                                                                                                                                                                                                                                                                                               Acetyl coenzyme A carboxylase; ACOACase; powdery mildew; fungus; ACCase; fatty acid biosynthesis; EC 6.4.1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microorganism with specific biochemical activity deleted by mutation and complemented, used in system to identify cpds with plant protecting activity, also new gene for acetyl coenzyme A carboxylase.
                                                Erysiphe graminis acetyl coenzyme A carboxylase
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                                                                                                                                                                                             AAR98811 standard; protein; 2273 AA.
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N-PSDB; AAT30758.
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10-FEB-1997
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65 FGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHA 124

64 86

Gaps

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Length 2273; Indels

Query Match
74.5%; Score 2166; DB 2;
Best Local Similarity 73.3%; Pred. No. 2.7e-193;
Matches 407; Conservative 61; Mismatches 87;

HKAVSOFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYET 

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184
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                                                                                                                              SDEGFEALYKAAANEIPGSPIFIMKLAGNARHLEVQLLADEYGNNISLFGRDCSVQRRHQ 326
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                                                                                                                                                                                                                KPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSOF 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted biotin binding domain and carboxy transferase domain, and having functional biotin carboxylase domain, useful for identifying ACCase inhibitors/activators.
VWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSG
                                            147 WWAGWGHASENPKLPESLAASPKKIVFIGPPGSAMRSLGDKISSTIVAQHAKVPCIPWSG
                                                                         TGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCT
                                                                                                                                                                                                                                                                                     NGEBFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQ
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                                                                                                                                                                                                    EHPTTEMVSGVNI PAAQLQVAMGI PLYSIRDIRTLYGNDPRGNEVIDFDFSSPESFKTQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel peptide (I) comprising an acetyl CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCase, Acetyl CoA carboxylase; carboxy transferase domain; biotin carboxylase domain; BC domain; fungicide; rice blast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M. grisea ACCase BC domain SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weatherly SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; SEQ ID NO 6; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-2002; 2002US-0401170P.
                                                                                                                                                                                                                                                                                                                                                                                                        ADJ47653 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                  545 QDRLTAERPPADLAV
                                                                                                                                                                                                                                                                                                                                                      567 SNKLTAERPDPTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CROP-) CROPSOLUTION INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Volrath SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-180421/17.
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carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxylase Gomain, and having a functional biotin carboxylase domain. A peptide of the invention is useful for identifying Acetyl CoA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA arboxylase inhibitor or activates.

The method further involves employing the identified binding compound in an assay to detect inhibition or enhancement of Acetyl CoA carboxylase carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity, A peptide of the invention is also useful for identifying fungicides, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, the presence of binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be fungicide, employing the identified compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound that inhibitis and a selecting a compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGIKETWMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCT 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 HKIADHFIGGNRLENAPPSKVKEWVAAHDGHTVITNVLIANNGIAAVKEIRSVRKWAYET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.4%; Score 2163; DB 8; 73.5%; Pred. No. 5.4e-194; ive 59; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                    represents an ACCase BC domain of the invention.
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promote for expression of a polymucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant ecombinant DNA construct and growing the transforming a plant with the recombinant DNA construct is useful for improving plant with the polymucleotide or polypeptide is useful for producing plant with the polymucleotide or polypeptide is useful for producing plant with the recombinant DNA construct is useful for producing plant with the polymucleotides, extreme osmotic conditions, pathogens or pests, increased resistance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or phosphorus use and/or uptake, by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved lignin production or improved glant growth and development under at least one stress condition, improved lignin production or improved glant members a bacterial polypeptide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                               carbohydrate;
                                                                                                                                             Recombinant DNA construct; transformed plant; improved plant property,
                                                                                                                                                                   osmosis;
                                                                                                                                                             cold tolerance; heat tolerance; drought tolerance; herbicide; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbo
                                                                                                                                                                                                                                                   nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          format from USPTO at segdata.uspto.gov/seguence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldman BS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 3698; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2002; 2002US-0360039P
                                                                                                     polypeptide #3698.
                                                              (first entry)
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HINKLE G
SLATER S
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                   ADN21045;
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Conservative

Matches 411;

Query Match Best Local Similarity

73.6%; Score 2139; DB 8; 68.8%; Pred. No. 9.5e-191; iive 58; Mismatches 86;

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42;

Indels

Length 2301;

Gaps --KVLI

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577 SKKLTAERPDKMLAV

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                                                                                                                                                                                                                                             SPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARES 322
                                                                                                                                                                                                                                                                               MEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQL 382
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                                                                                                                                              Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; plant tolerance; heat tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
ANNGIAAVKEIRSVRKWAYETFGDERAIKFTVMATPEDLQANADYIRMADHYVEVPGGTN
                                                                                               AASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSD
                                   CNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSN
                                                                                 NNNYANVDLI VDVAERAGVHAVWAGW---------GHASENPRLPESL
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CAO Y.
HINKLE G J.
SLATER S C.
CHEN X.
GOLDMAN B S.

(CAOY/) (HINK/) (SLAT/) (CHEN/) (GOLD/)

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a plant with the recombinant DNA construct and growing the transformed plant, where the complication dor polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with the improved plant properties, e.g. improved cold, heat or drought tolerance, collerance to herbicides, e.g. improved cold, heat or drought tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or content, improved yield by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and envelopment under at least one stress condition improved plant growth and envelopment under at least one stress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                         New recombinant DNA construct comprising a promoter positioned to provifor expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTIDEETWIVITVDDDVYQXACIRSAEEGIAVAEKIGYPVMIKASEGGGGGGGIROVISTE
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EEAPVIIAPAATFHEMERAAVRLGELVGYASAGTIEYLYEPENDRFYFLELNPRLQVEHP
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                     BS;
                       Goldman
                                                                                                                                                                                             Claim 1; SEQ ID NO 2130; 122pp; English
                     Chen X,
                  Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 71.4 Matches 394; Conservative
                                                               WPI; 2004-061375/06
                  Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2241 AA;
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Saccharomyces cerevisiae
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         FAYGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDR 547
                    70 SHFLGGNSVLNAEPSKVRDFVRAHQGHTVISKILIANNGIAAVKEIRSVRKWAYETFGDE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                 A polynucleotide encoding an Acetyl-COA carboxylase gene from Candida albicans overexpressed in Saccharomyces cerevisiae for purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDE
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                                                                                                                                                                                                                    Candida albicans; acetyl CoA carboxylase; ACCase.
                                                                                                                                                                                                                                                                                                                                                                            Thain JL,
                                                                                                                                                                                              Candida albicans acetyl CoA carboxylase.
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                                                                                                                              AAY24150 standard; protein; 2270
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541 VTSARPDKMLAV
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                                                   LTAERPPADLAV
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N-PSDB; AAX88525.
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Best Local Similarity
Matches 390; Conserv
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                                                                                                                                                                                                                                          Candida albicans
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190 WGHASENPLLPEKLAASPKKIIFIGPPGSAMRSLGDKISSTIVAQHAQVPCIPWSGTGVD 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted biotin binding domain and carboxy transferase domain, and having functional biotin carboxylase domain, useful for identifying ACCase inhibitors/activators.
                                                                                                                      | : |:||:|||||| : EVKIDPQTNLVSVADDIYAKGCCTSPEDGLEKAKKIGFPVMIKASEGGGGKGIRKVDDEK
                                                                                                                                                                                                                                       310 NFITLYNQAANEIPGSPIFIMKLAGDARHLEVQLLADQYGTNISLFGRDCSVQRRHQKII
                                                                                                                                                                                                                                                                                                                                                          ETMMSDQ-GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGE
                                                                                                                                                                                                   248 EFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKII
                                                                                                                                                                                                                                                                                                                              EEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 TTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           488 FAYGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIODR
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biotin carboxylase domain; BC domain; fungicide.
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Multiprotein complex; eukaryote; drug target; diagnosis

cerevisiae

Saccharomyces SP1258494-A1

Protein sequence #SEQ ID 325

20-JUN-2003

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CC Acetyl CoA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase domain, determining whether or not the compound binds compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding compound in an assay to detect inhibition or enhancement of Acetyl CoA carboxylase cortivity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity. A peptide of the invention is also useful for identifying fungicides, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or carboxylase domain, the presence of binding indicating the compound carboxylase activity, and selecting a compound that inhibition of Acetyl CoA carboxylase activity, and selecting a compound carboxylase activity. The present sequence that inhibits Acetyl CoA carboxylase activity. The present sequence
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Matches 386; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 580 AA;
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or

New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease disorder.

Disclosure; SEQ ID NO 325; 17pp + Sequence Listing; English.

Kruse UD, Kuester

i P, Krause R, K Superti-Purga GD;

Grandi P,

Bauer A, Gavin A, Grand Marzioch M, Schultz JD,

WPI; 2003-250078/25.

N-PSDB; ACC60772

15-MAY-2001; 2001EP-00111774.

(CELL-) CELLZOME AG

20-DEC-2001; 2001EP-00130253

20-NOV-2002

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The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distainor proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the Buropean Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKCTNGEEFKQLYNAVLGEVPGSPVFVMKCLAGQARHLEVQLLADQYGNAISIFGRDCSVQ 300
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nes 386; Conservative
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ABR52730

RESULT 9
ABR52730
ID ABR5
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AC ABR5:
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us-10-633-835-2.rag

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second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the protein second protein complexes, which are not defined to in the specification. The variants are encoded by nucleic acids that the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for the presence of a disorder the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was
 RLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESF 420
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                                                                                                                                                  The invention relates to novel protein complexes comprising a first and a
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                                                                KTORKPOPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New proteins and protein complexes from eukaryotes, useful as targets drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G, Kuester B, Schultz J;
Kruse U, Merino A, Bauch A;
                                                                                                                                                                                                                                                                                                                                                                                                             protein #110
                                                                                                                                                                                                                                                                                                                                                                                                             treating protein complex-derived
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P, Krause R,
IC, Rick J;
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| DDLITHKMTAEKPDPTLAV 581
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n M, Grandi E
A, Leutwein C
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N-PSDB; ADK61969.
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metabolic syndrome; diabetes; obesity; cardiovascular disease;
atherosclerosis; depression; cancer; hyperlipidaemia; dyslipidaemia;
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                                                Length 2000;
                                                                        Indels
                                                70.9%; Score 2060; DB 7; 69.1%; Pred. No. 2.1e-183;
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hypertension, hyperuricaemia, renal disfunction,
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from the BPO in electronic format)
                                                            69.1%; Pred. No. 2.1e
ive 76; Mismatches
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                                                            Best Local Similarity
Matches 386; Conserv
                       Sequence 2000 AA;
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New crystallizable composition comprising a carboxyltransferase domain of acetyl-coenzyme A (COA) carboxylase, for treating e.g. diabetes, obesity, cardiovascular disease, atherosclerosis, or cancer.
                                                                                                                                                                                                                                                                                     The invention comprises a crystallisable composition containing a carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-COA) carboxyltranse. The composition of the invention is useful for treating: metabolic syndrome, diabetes, obesity, cardiovascular disease, atherosclerosis, depression, cancer, hyperlipidaemia, dyslipidaemia, hypertension, hyperuricaemia and renal disfunction. The present amino acid sequence represents a yeast acetyl-CoA carboxylase of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 DAVWAGWGHASENPLLPEKLSQSKRKVIFIGPPGNAMRSLGDKISSTIVAQSAKVPCIFW 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKCTNGEBFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             70.9%; Score 2060; DB 8; 69.1%; Pred. No. 2.5e-183; ive 76; Mismatches 89;
                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 1; 195pp; English
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DDLITHKMTAEKPDPTLAV 581
                                                                                                    (UYCO ) UNIV COLUMBIA NEW YORK.
                            31-MAR-2003; 2003US-0459464P.
31-JUL-2003; 2003US-0491640P.
27-OCT-2003; 2003US-0514656F.
09-JAN-2004; 2004US-00514636.
               2003US-0439383P
                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.1%;
                                                                                                                                    Zhang H, Yang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 69.1
Matches 386; Conservative
                                                                                                                                                                  WPI; 2004-571486/55.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2233 AA;
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cold tolerance, heat tolerance, drought tolerance, herbicide, osmosis, pathogen tolerance, pest tolerance, plant disease resistance; cell cycle pathway modification, plant growth regulator; homologous recombination, seed oil yield; protein yield; carbohydrate, nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide. Recombinant DNA construct; transformed plant; improved , Goldman Chen X, Z protein; 2233 Hinkle GJ, Slater SC, 21-FEB-2002; 2002US-0360039P. 20-FEB-2003; 2003US-00369493 Bacterial polypeptide #1998. (first GOLDMAN B S. ADN19345 standard; نن CAO Y. HINKLE G J SLATER S C US2003233675-A1 CHEN 02-DEC-2004 18-DEC-2003 ADN19345; Bacteria, SLAT/) GOLD/) (CAOY/) (HINK/) Cao Y, ADN19345 

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties. WPI; 2004-061375/06.

143

62 83

Gaps 8

Length 2233;

240 262 322

382 420 480 502 540 562

Claim 1; SEQ ID NO 1998; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymuclectide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant the combinant DNA construct and growings the transformed plant with the recombinant DNA construct is useful for improving plant where the polymuclectide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with the improved plant properties, e.g. improved cold, heat or drought tolerance. The recombinant DNA construct assembly to producing plants with inproved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan or production. This sequence represents a bacterial polypeptide used in the condition. patent did not scope of the invention. Note: The sequence data for this patent did no form part of the printed specification but was obtained in electronic format from USPTO at sequata.uspto.gov/sequence.html.

Sequence 2233 AA;

Query Match

Length 2233, DB 8; Score 2060; 70.9%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                     RRHOKIIEBAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNP
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                                        PDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAY
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                    Gaps
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                  Indels
        ed. No. 2.5e-183;
Mismatches 89;
        Pred.
69.1%; F. 76;
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DDLITHKMTAEKPDPTLAV
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                   Conservative
         Similarity
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant comprising the recombinant DNA construct and growing the transforming a plant with the recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for improving plant properties. Colerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant showth and development of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant showth and development of photosynthesis or by production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form at norm at norm of the condition of the printed specification because obtained in electronic
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                                                                                                                                                                                             promoter positioned to provide
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                                                                                                                                                                                                                 for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94;
                                                                                                        Goldman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 65.0%; Score 1889.5; DB 8
Best Local Similarity 64.3%; Pred. No. 7.3e-168;
Matches 355; Conservative 86; Mismatches 94;
                                                                                                                                                                                           comprising a
                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1905; 122pp; English.
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                                                                                                        Chen
                                                                                                        SC,
                                                                                                                                                                                             New recombinant DNA construct
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PRLOVEHPTTEMVSGVNIPAAOLOVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPES

458

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Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
Michon A, Leutwein C, Rick J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disease treating protein complex-derived protein #1382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein complex; drug target; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                       ADK63986 standard; protein; 2000 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                LDGLIQDRLTAE 551
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N-PSDB; ADK63987.
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targets in New proteins and protein complexes from eukaryotes, useful as targets drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or disorder in a subject

Disclosure; SEQ ID NO 2763; 13pp; English.

second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that. Thy pridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this petern did not form part of the printed specification but was The invention relates to novel protein complexes comprising a first and a EPO in electronic format)

Sequence 2000 AA;

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158
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                                                                                             YETFGDERAIBFTVWATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAG 121
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                                                                                                                                               VHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMP
                                                                                                                                                                                             WSGTGIKETWMSDQ--GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKG
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   Length 2000;
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                          Indels
                          94;
  5; DB 7
Query Match 65.0%; Score 1889.5; Best Local Similarity 64.3%; Pred. No. 2.4e Matches 355; Conservative '86; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ACC1 BC domain SEQ ID NO:10.
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The invention relates to a novel peptide (I) comprising an acetyl CoA carboxylase (AcCase) having a deleted biotin binding domain, having a dieleted carboxylase (arboxylase domain, and having a functional biotin carboxylase domain. A peptide of the invention is useful for identifying Acetyl CoA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding compound in a say to detect inhibition or enhancement of Acetyl CoA carboxylase (C) an assay to detect inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity. A peptide of the invention is also useful for identifying fungicides, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase commain, determining whether or not the compound binds to the biotin carboxylase domain, the presence of binding indicating the compound is or carboxylase domain, the presence of binding indicating the compound cin an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound that inhibits Acetyl CoA carboxylase activity, and selecting equence that inhibits Acetyl CoA carboxylase activity, and selecting equence of compound that inhibits Acetyl CoA carboxylase activity, and selecting equence of that inhibits Acetyl CoA carboxylase activity, and selecting equence of page activity, and selecting the present sequence of represents the human ACC1 BC domain.
                           eptide comprising acetyl CoA carboxylase (ACCase) having deleted binding domain and carboxy transferase domain, and having anal biotin carboxylase domain, useful for identifying ACCase
                                                                                                                                                                                              Claim 9; SEQ ID NO 10; 56pp; English.
                                                                                                                               inhibitors/activators
                                                                                                Functional
                                                                 biotin
                                  Novel
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61.6%; Score 1790; DB 8; Length 632; 63.8%; Pred. No. 8.2e-159; Matches 345; Conservative Local Similarity Sequence 632 AA; Query Match

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400 VFEHMEQCAVKLAKMGYVSAGTVEYLYS-QDGSFYFLELMPRLQVEHPCTEMVADVNLP 458 438 511 498 161 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QGFL 198 TVSDDVYQQACIHTAEEGLEXAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLG 258 EVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPED 318 572 SNAVVALKELSIRGDFRTTVEYLIKLIETESFOMMRIDTGWLDRLIAEKVOAERPDTMLG 631 LKVNADYIRMADOYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141 EVPGSPIFVMRLAKOSRHLEVQILADOYGNAISLFGRDCSVQRRHQKIIEEAPATIATPA 399 81 ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIP AAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRIT AAQLQIAMGIPLYRIKDIRMMYGVSPWGDSPIDFEDSA-----HVPCPRGHVIAARIT AENPOTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR SENPDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFADSQFGHCFSWGENREAI KOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLA Gaps 14; 63.8%; Pred. No. 5.25.103; Indels ive 79; Mismatches 103; Indels 499 22 103 82 142 222 199 280 259 340 379 459 439 162 g 셤 g 원 g 셤 셤 硆 ઠે ઠે ò ò ઠે δ

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The invention comprises a crystallisable composition containing a carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-COA) carboxylase. The composition of the invention is useful for treating: metabolic syndrome, diabetes, obesity, cardiovascular disease, atherosclerosis, depression, cancer, hyperlipidaemia, dyalipidaemia, hyperunicaemia and renal disfunction. The present amino acid sequence represents a human acetyl-COA carboxylase of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New crystallizable composition comprising a carboxyltransferase domain of acetyl-coenzyme A (COA) carboxylase, for treating e.g. diabetes, obesity, cardiovascular disease, atherosclerosis, or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 LKANAEYIKWADHYVPVPGGPNNNNYANVELILDIAKRIPVQAVWAGWGHASENPKLPEL 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES
                                                                                                                                                                                                                                          acetyl-coenzyme A carboxylase; acetyl-CoA carboxylase; metabolic syndrome; diabetes; obesity; cardiovascular disease; atherosclerosis; depression; cancer; hyperlipidaemia; dyslipidaemia; hypertension; hyperuricaemia; renal disfunction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.5%; Score 1787; DB 8; 63.6%; Pred. No. 1.4e-157; ive 79; Mismatches 104;
                                                                                                                                                                                                                               carboxyltransferase domain; CT domain;
                                                                                                                                                                                                  Human acetyl-coenzyme A carboxylase - ACC1.
                                                                                                                                                                                                                                                                                                         crystallisable composition; enzyme; ACC1.
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                                                                                                      ADQ90744 standard; protein; 2346 AA
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2003US-0491640P.
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les 344; Conservative
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The present sequence represents human acetyl coenzyme A-carboxylase alpha (ACC-alpha). The ACC-alpha protein was used in the course of the invention. The specification describes a molecular complex comprising a polypeptide having amino acids 1640-1663 of the human BRCAl protein (or
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N-PSDB; ABZ23503.
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similar sequence from some other animal species), and a polypeptide that is a part of the accetyl coenzyme A-carboxylase alpha (ACC-alpha) protein able to bind the BRCAl protein. The complex is implicated in predisposition to cancer of breast and ovary. It is used to screen for compounds that modulate interaction between BRCAl and ACC-alpha, which are potentially useful for treatment, prevention and diagnosis of cancer, and to identify endogenous ligands. Modulated formation of the complex of an be used for diagnosis of cancer. Antibodies directed against specific parts of human ACC-alpha are useful for localization of the complex in cells
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63.6%; Pred. No. 5.2e-157;
ive 79; Mismatches. 104; Indels
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The present sequence is the protein sequence for human acetyl-Coenzyme A-carboxylase-alpha (ACC-alpha). This sequence can be used for in vitro diagnosis of cancer (or of an increased risk of developing it), by detecting ACC-alpha gene mutations or polymorphisms, or altered ACC-alpha protein expression, relative to a control population. The method is particularly used to diagnose cancer, especially of breast or ovary, or for assessing the risk of developing such cancers
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63.6%; Pred. No. 5.2e-157;
ive 79; Mismatches 104;
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Matches 344; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QGFL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVLG 258
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                                                                                                                                                                                                                                                                                                                                                         cancer, or coenzyme A-
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                                                                                                                                                                                                                                                                                   Sinilnikova-Erard
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                                  /note= "Leu substituted with Val"
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                                                                                                                                                                                                                                                                                   Lenoir GM,
Location/Qualifiers
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UNIV LYON 1 BERNARD CLAUDE.
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2002FR-00002788
                                                                                                                                         2002WO-FR002015
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 Key
Misc-difference
                                                                       WO2002100896-A2
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05-MAR-2002;
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diagnosis of cancer (or of an increased risk of developing it), by detecting ACC-alpha gene mutations or polymorphisms, or altered ACC-alpha protein expression, relative to a control population. The method is particularly used to diagnose cancer, especially of breast or ovary, or for assessing the risk of developing such cancers. Note: The present sequence was not shown in the specification, but was derived from information given

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Gaps

14;

Length 2346; Indels

Sequence 2346 AA;

LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141 

ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED

22 103 82 162 142

198

LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD----QGFL

280 NVPQELYEKGYVKDVDDGLKAAEKVGYPVMIKASEGGGGKGIRKVNNADDFPNLFRQVQA 339

319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP 379 AAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRIT 439 AENPDIGFKPGMGALTELNFRSSISTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR 499 KOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLA

**EVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPED** 

TVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLG 258

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SIMVVALKELSIRGDFRITVEYLIKILETESFQMNRIDTGWLDRLIAEKVRAERPDTMLG

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Query Match 61.3%; Score 1781; DB 6; Best Local Similarity 63.6%; Pred. No. 5.2e-157; Matches 344; Conservative 79; Mismatches 104;
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         TVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLG 258
                                                                                                                             319 ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP 378
                                                                                                                                                                                                                        AAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRIT 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLA 558
                                  ORRHOKIIEEAPVTIAPED
                                                                                                                                                                                                                                                                                                                                                                                                                  SENPDEGFKPSSGTVQELNFRSNRNVWGYFSVAAAGGLHEFAGSQFGHCFSWGENREEAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human acetyl-Coenzyme A-carboxylase-alpha variant #2
                                                                                                       EVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCS
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2271
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developmental biology; cell signalling; insecticide;
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                                    ABB59490 standard; protein; 2348
                                                               (first entry)
                                                                                                               Drosophila melanogaster.
  632
                                                                                                  pharmaceutical
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                                                               26-MAR-2002
                                                                                           Drosophila;
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                                                 ABB59490;
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                     RESULT 21
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cancer, or coenzyme A-

Sinilnikova-Erard

Lenoir GM,

Magnard CM,

WPI; 2003-175165/17. Dalla Venezia NL,

in vitro

CENT NAT RECH SCI. LYON 1 BERNARD CLAUDE.

(CNRS ) CNRS (UYLY-) UNIV

2002WO-FR002015

12-JUN-2002;

13-JUN-2001; 2001FR-00007740. 05-MAR-2002; 2002FR-00002788.

In vitro diagnosis of cancer, particularly breast and ovarian susceptibility, comprises detecting alterations in the acetyl carboxylase alpha gene or protein expression.

27-SEP-2001

The present sequence is a variant sequence for human acetyl-Coenzyme A-carboxylase-alpha (ACC-alpha). This sequence can be used for in vitro

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAM 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                582
                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABBS7737-ABR20772). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                            DYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV
                                                                                                                                                                                                                                                                                                                                             2348;
                                                                                                                                                                               Disclosure; SEQ ID NO 5262; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                           ; Score 1780; DB 4;
; Pred. No. 6.5e-157;
69; Mismatches 110;
                                                                                  E.
                                                                                   Myers
                                                                                  PWD,
                                                                                                                                                                                                                                                                                                                                           61.2%;
                              23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
        23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                 ቷ
                                                                                  Adams M,
                                                                                                       WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                            (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                        Sequence 2348 AA
                                                                                                                  ABL03593
                                                                                                                                                            interactions
                                                                                                                                                                                                                                                                                                                                                                 342;
                                                                                Venter JC,
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                                                                                                                  N-PSDB;
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Matches
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Lue present invention provides the protein and coding sequences of the Drosophila melanogaster acetyl CoA carboxylase enzyme (ACCase). The sequences can be used to identify insecticidal and acaricidal agents that act by modulating activity or expression of ACCase. The present sequence is the protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding insect acetyl-coenzyme A carboxylase, useful for identifying insecticidal and acaricidal agents, also related proteins and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetyl CoA carboxylase; enzyme; ACCase; insect; fruit fly; insecticide; acaricide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 DYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 HKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 AVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIPAAQLOVAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 GIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 DFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.2%; Score 1780; DB 5; 64.2%; Pred. No. 6.5e-157; ive 69; Mismatches 110;
                                                                                                                       Drosophila melanogaster Acetyl-CoA carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Teuschel
Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 21-28; 34pp; German.
AAO19075 standard; protein; 2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nauen R,
                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-2000; 2000DE-01062422
                                                                                                                                                                                                                                                                                                                                                    14-DEC-2000; 2000DE-01062422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity 64.2
342; Conservative
                                                                                                                                                                                                                           Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAL49486
                                                                                                                                                                                                                                                                    DE10062422-A1
                                                                              14-NOV-2002
                                                                                                                                                                                                                                                                                                             20-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
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The invention relates to a novel nucleic acid (I) comprising (i) a 4047 bp sequence (ABN85738) or AAF59156; (ii) a segment with at least 14 bp from (i); (iii) a sequence that hybridizes to (i) or (ii) at 37-50c; (iv) a sequence at least 60% identical with (i) or (ii); (v) a complement of (i)-(iv) or (vi) an equivalent of (i)-(iv) within the degeneracy of the genetic code. (I) and the encoded polypeptide (II, ABB83866) having ACCase (acetyl-CoA carboxylase, EC 6.4.1.2) activity are used to identify insecticidal and acaricidal agents that eact by modulating activity or expression of ACCase, an essential enzyme for survival of insects. The present sequence is that of the Drosophila melanogaster ACCase of the
                                          KPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLK 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding insect acetyl-coenzyme A carboxylase, useful for identifying insecticidal and acaricidal agents, also related proteins and modulators.
                                                         Drosophila melanogaster; fruit fly; Acetyl-CoA carboxylase; ACCase; insecticide; acaricide; EC 6.4.1.2; enzyme.
                                                                                                     559
                                                                                                                 BLSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV
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Pred. No. 6.5e-157;
69; Mismatches 110;
                                                                                                                                                                                                                                                                                          Drosophila melanogaster ACCase SEQ ID NO 2.
|||||| ::||| ||| | ::||||:
GIPLYRLKDIRLLYGESPWGSSVIDFE-
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                                                                                                                                                                                                   ABB83866 standard; protein; 2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Teuschel U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-DEC-2000; 2000DE-01062421
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64.2%;
                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-584630/63.
N-PSDB; ABN85738.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2348 AA;
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                                                                     523
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                                                                                                                                                                                                                                  ABB83866;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bovine acetyl coenzyme A carboxylase alpha gene (Accalpha), or its fragments, which are used to control expression of foreign genes. When the promoter (or the Accalpha structural gene) is replaced, at least in part, by a sequence that is altered by deletion or substitution, then expression of Accalpha in the milk gland is reduced and the milk produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acetyl-coenzyme A carboxylase-alpha; acetyl-coA carboxylase alpha; bovine; milk gland-specific promoter; Accalpha; milk production; sheep; goat; fat content; genotyping; lactation.
147 HKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQ
                                                                                                                                                                                                                                                                                                      291 RGCVTNVEQGLAAVNKIGFPVMIKASEGGGGKGIRRVDTTEEFPGLFRQVQAEVPGSPIF
                                                                                                             VMKLAGQARHLEVQLLADQYGNAISIPGRDCSVQRRHQKIIEBAPVTIAPEDARESMEKA
                                                                                                                               AVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI PAAQLQVAM
                                                                                                                                                                                                                                                         470 GIPLYRLKDIRLLYGESPWGSSVIDFE-----NPPNKPRPSGHVIAARITSENPDEGF
                                                                                                                                                                                                                                                                                     KPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKQMVISLK
                                                                                                                                                                                                                              GIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel milk gland-specific promoter of the
                                                                                                                                                                                                                                                                                                                                                559
                                                                                                                                                                                                                                                                                                                                                                            635
                                                                                                                                                                                                                                                                                                                                              ELSIRGDFRITVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADLAV
                                                                                                                                                                                                                                                                                                                                                               Bovine acetyl-coenzyme A carboxylase-alpha protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB86033 standard; protein; 2288
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DYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASK

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12;

Indels

Best Local Similarity 64.2 Matches 342; Conservative

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ABM83569 standard; protein; 2420 AA
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(by cattle, sheep or goats) has reduced fat content. Analysis of the polymorphic 933-966 region of (Accalpha) is useful for genotyping animals, producing a genotype that is directly correlated with Accalpha expression during lactation and with fat content of the milk. This makes it possible to generate populations of cattle that produce milk of high or low fat content by classical breeding methods. Accalpha is a lactation specific, inducible promoter for expressing foreign proteins in the milk and, when modified, results in milk of reduced fat content, which facilitates recovery of proteins. This sequence represents a fragment from bovine Accalpha which contains a fragment of exon 5A exon 6 and exon
                                                                                                                                                                                                                                                                             AEVPGSPIFVMRLAKQSRHLEVQILADQYGNAISLFGRDCSVQRRHQKIIEEAPAAIATP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVFEHMEQCAVKLARMVGYVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPCTEMVADVNL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437
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                                                                                                                                                                                                                                                                                                               LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGI----KETWMSDQGF 197
                                                                                                                                                                                                                                                                                                                                    LL--KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSGSGLCVDWHENDFSKR-I 220
                                                                                                                                                                                                                                                                                                                                                                                                          GEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAENPOTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 ISNMVVALKELSIRGDFRTTVEYLIKLLETESFQLNRIGTGWLDRLIAEKVQAERPDTML 572
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                                                                                                                                                                                                                               ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                                                                                                                                               LKVNADY I RMADQYVEVPGGSNNNNYANVDL I VDVA ERAGVHAVWAGWGHAS ENPRLPES
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                                                                                                                                                                                           Gaps
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                                                                                                                                                                  Length 2288;
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                                                                                                                                                                                          Indels
                                                                                                                                                                 Query Match 61.1%; Score 1775; DB 4;
Best Local Similarity 63.7%; Pred. No. 1.8e-156;
Matches 345; Conservative 78; Mismatches 103;
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(first entry)
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16-AUG-1990
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280 NVPQELYEKGYVKDADDGLRAAEEVGYPVMIKASEGGGKGIRKVNNADDFPNLFRQVQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 AAQLQVAMGIFLYSIRDIRTLYGMDFRGNEVIDFDFSSFEFKTQRKPQPQGHVVACRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 AENPOTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR
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                                                                                                                                                                                                                                    has
                                                                                                                                                                                                                                                                                                                              derived from chicken liver. (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                  from chicken liver,
                                                                                                                                                                                                                                                                                                                                                                                                                  61.0%; Score 1774; DB 2;
63.0%; Pred. No. 2.3e-156;
ive 83; Mismatches 103;
                                                                                                                                                                                                                                                                                            Japanese
                                                                                                                                                                                                                                      - derived
                                                                                                                                             (MEIP ) MEIJI MILK PROD CO LTD
                                                                                                          88JP-00208170
                                                                                                                                                                                                                                                                                          Disclosure, Fig 2, 14pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                    Acetyl-coa-carboxylase - and amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2324 AA;
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JP02057179-A.
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Best Local Simil
Matches 341;
                                                                                                          24-AUG-1988;
                                                                        24-AUG-1988;
                                      26-FEB-1990
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LTVSDDVYQQACIHTABEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL 257 

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542 AIPEFMEQCAIRLAKTVGYVSAGTVEXLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL 318 DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI

437 ITAENPOTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSE **ARKOMVISLKELSIRGDFRITVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPAD** 

LGV 775

PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKT-QRKPQPQGHVVACR

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652 496 712 556

377

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(first entry)

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gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                  Human diagnostic and therapeutic pprotein SEQ ID NO:3818.
                                                              12-SEP-2002; 2002US-0410259P.
                                                       12-SEP-2003; 2003WO-US028227
                                                                          (INCY-) INCYTE CORP.
                                        WO2004023973-A2.
                                 Homo sapiens
           18-NOV-2004
                                               25-MAR-2004.
    ABM83569
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ABP59211 standard; protein; 2458 557 LAV 559 10-MAY-2003 497 ABP59211; 773 RESULT 27 ABP5921 a ਨੇ 셤 ð The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A polymucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated to with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorders, or disorder, neurological disorders, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm Gietzen D; 303 LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QG-F 197 New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping. 81 ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED Wright RJ, Bruns CM, Marjanovic MM, Shen F;
2 TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Blanchard JL, Panzer SK, Wang X, Au AP, Gerstin EH;
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirron ES;
99 M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzé Gaps 17; DB 8; Length 2420; Indels 101; 60.9%; Score 1769.5; DB 8 63.4%; Pred. No. 6.6e-156; iive 75; Mismatches 107; Claim 27; Page; 190pp; English. Suarez CJ; Best Local Similarity 63.4 Matches 344; Conservative 2004-329368/30. Kwong M, Po S, Shi X, Sequence 2420 AA; N-PSDB; ACN42221 Stevens KA, Peralta CH, Lagace RE, S Harthshorne Schmidt JP, Patury S, Mooney EM, 22 245 304 142 82 Query Match

(first entry)

Human; drug metabolising enzyme; anti-HIV; antiallergic; antidiarrheic; antilnflammatory; antianaemic; thrombolytic; antilipaemic; antidiarrheic; antiarteriosclerotic; antiasthmatic; immunosuppressive; antityroid; cytostatic; hepatotropic; virucide; dermatological; antidiabetic; nephrotropic; antigout; neuroprotective; thyromimeic; osteopathic; antiarthritic; antipsoriatic; uropathic; ophthalmological; antirheumatic; haemostatic; gene therapy; cell proliferative disorder; cancer; developmental disorder; endocrine disorder; eye disorder; automatoric; metabolic disorder; pastrointestinal disorder; liver disorder; autoimmune disorder; inflammatory disorder; DME-2. Elliott VS; Emerling BM, Richardson TW, Li JX, Baughn MR, Tang YT, Lee EA, Elliott VS A, Porsythe IJ, Sanjanwala MM, Yao MG; Burford N; Human drug metabolising enzyme, DME-2, SEQ ID 2. Swarnakar A, Folding... 06-JUL-2001; 2001US-0303745P. 13-JUL-2001; 2001US-0305402P. 27-JUL-2001; 2001US-0308158P. 14-SEP-2001; 2001US-0322127P. 05-JUL-2002; 2002WO-US021105 (INCY-) INCYTE GENOMICS INC. Ramkumar J, Honchell CD, WO2003004608-A2. κ'χ Homo sapiens. Warren BA, F Yue H, Lee S Zebarjadian Y Griffin JA, 16-JAN-2003.

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The present invention relates to novel human drug metabolising enzymes, DME-13 (ABP59210-ABP5922) and their coding sequences (ABZ81301-ABZ81313). The sequences are useful for diagnosing, treating or preventing disorders associated with aberrant expression of DME, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, paroxyman incutural haemoglobinuria, polycythaemia vera, psoriasis, paroxyman incutural haemoglobinuria, polycythaemia vera, psoriasis, paroxyman incutural haemoglobinuria, colycythaemia vera, psoriasis, paroxyman incutorine, eng. sereoporosis, thrombocytopenia or mental creatadrion), endocrine (e.g. osteoporosis, thrombocis, diabetes), eye disorders (e.g. glaucoma, keratitis), metabolic (e.g. hyperlipidaemia, cystic fibrosis), gastrointestinal disorders (e.g. hyperlipidaemia, cystic fibrosis), jastrointestinal disorders (e.g. hyperlipidaemia, outcimmune thyroiditis, contact dermatitis, Crohn's disease, auttoimmune thyroiditis, contact dermatitis, Crohn's disease, osteoarthritis, pancreatitis, Reter's syndrome, multiple sclerosis, osteoarthritis, pancreatitis, Reter's syndrome, multiple sclerosis, sloperen's syndrome, uveitis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, pancreatitis, Reter's syndrome, rheumatoid arthritis, strongenous compounds on the expression of nucleic acid and amino acid sequences of DME. The polymucleotides encoding DME are useful correating transgenic animals to model human disease
                                                                                New drug metabolizing enzymes (DME) useful for diagnosing, treating preventing diseases or conditions associated with aberrant DME expression, e.g. cancer, AIDS, atherosclerosis, diabetes, glaucoma, hepatitis or osteoporosis.
                                                                                                                                                                                                                                     Claim 1; Page 149-155; 181pp; English.
WPI; 2003-221588/21
                        N-PSDB; ABZ81302
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Sequence 2458, AA;

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245 ASP-AEFVTRFGGDRVIEKVLIANNGIAAVKCMRSIRRWAYEMFRNERAIRFVVMVTPED 303
                                                                                                                                          542 AIFEFWEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL 600
                                                                                                                         LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                                                                                                                    LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QG-F 197
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                                                            22 ASPVADFIRKOGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
60.9%; Score 1769.5; DB 6; Length 2458; 63.4%; Pred. No. 6.8e-156; ive 75; Mismatches 107; Indels 17;
              Best Local Similarity 63.4
Matches 344; Conservative
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Secreted protein; SECP; human; antiarteriosclerotic; antiatherosclerotic; hepatotropic; cytostatic; anti-HIV; antiallergic; antiaschmatic; cancer; antianemic; antialabetic; antiallergic; antianemic; antialabetic; antialammatory; neuroprotective; antiulcer; antiathermatic; cardiant; hypotensive; gonadal dysgenesis; vasotropic; anticonvulsant; nootropic; immunosuppressive; pericarditis; antiparkinsonian; ophthalmological; cell proliferative disorder; arteinsoclerosis; arteinsoclerosis; crimtosis; hepatitis; angina pericardicis; autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy; ulcerative colitis; cardiovascular disorder; myocarditis; nooraditis; huntington's disease; Malheimer's disease; Crentzfeldt-Jakob disease; developmental disorder; puchenne muscular dystrophy; antipsoriatic;
                                                                                                                                            Human SECP-1 protein from clone 7757335CD1 SEQ ID 1.
                                                                                                                                                                                                                                                                                                       Becker muscular dystrophy; Cushing's syndrome
                                                                            ABB84649 standard; protein; 2487 AA.
                                                                                                                        (first entry)
                      775
 559
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                      16
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                      773
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557
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WO200279441-A2 Homo sapiens

10-0CT-2002

2001US-0280527P. 2001US-0282112P. 2001US-0283702P. 2001US-0283855P. 2001US-0343718P. 2001US-0339236P. 2002US-0357002P. 29-MAR-2002; 2002WO-US009820 30-MAR-2001; 06-APR-2001; 13-APR-2001; 19-OCT-2001; 07-DEC-2001; 13-FEB-2002;

(INCY-) INCYTE GENOMICS INC.

Baughn MR, Burford N, Ding L, Duggan BM, Elliott VS, Forsythe IJ; Gandhi AR, Gietzen KJ, Griffin JA, He A, Honchell CD, Ison CH; Lal PG, Lee EA, Lee S, Lu DAM, Mason PM, Sanjanwala MM; Swarnakar A, Ramkumar J, Tang YT, Thangavelu K, Tran UK, Walia NK; Warren BA, Yao MG, Xu Y, Yue H;

WPI; 2003-058429/05. N-PSDB; ABS57545 Novel human secreted protein useful for treating, preventing or diagnosing cancer, hepatitis, psoriasis, asthma, diabetes mellitus, anemia, epilepsy, cataract, Alzheimer's disease.

Claim 56; Page 143-149; 188pp; English.

antiatreriosclerotic, antiatherosclerotic, hepatotropic, cytostatic, antiatherosclerotic, antiatherosclerotic, antiatherosclerotic, antiatherotic, antiatherotic, antiatherotic, antiatherotic, antiatherotic, antiatherotic, antiatherotic, antiatherotic, cardiant, hypotensive, anticonvulsant, nootropic, immunosuppressive, antiparkinsonian and ophthalmological activity. The polymucleotides and polypeptides of the invention can be used for diagnosing, treating or preventing cell proliferative disorder e.g. arteriosclerosis, atherosclerosis, cirthosis, hepatitis, cancer, autoimmune/inflammatory disorders e.g. acquired immunodeficiency syndrome This invention describes novel secreted proteins (SECP) which

Human NOV76a protein.

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cataract, gonadal dysgenesis, Cushing, sporiasis, rheumatoid arthritis, multiple sclerosis, ulcerative colitis, psoriasis, rheumatoid arthritis, etc; cardiovascular disorder e.g. myocardial infarction, angina pectoris, hypertension, Raynaud's disease. myocardial infarction, angina pectoris, hypertension, Raynaud's disease, myocarditis, pericarditis, etc; neurological disorders e.g. epilepsy, Huntingron's disease, Parkinson's disease, Albahimer's disease, Parkinson's disease, Albahimer's disease, Parkinson's cataract, gonadal dysgenesis, Cushing's syndrome, etc. The products of the invention can also be used for drug screening, proteome analysis, microarrays creating knock-in humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridization probes for mapping naturally occurring genomic sequences. ABB84649-ABB84673.

Crepresent secreted proteins encoded by the cDNA's shown in ABS57545-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QG-F 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 LTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKVNADYIRMADOYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 LC--RNGVAFLGPPSEAMWALGDKIASTVVAQTLQVPTLPWSGSGLIVJEWTEDDLQQGKR 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 GEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPE 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542 AIPERMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL 600
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                                                                                                                                                                                                                                                                                                                                                                                               60.9%; Score 1769.5; DB 6; Length 2487; 63.4%; Pred. No. 6.9e-156; i.ve 75; Mismatches 107; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.9%
Best Local Similarity 63.4%
Matches 344; Conservative
                                                                                                                                                                                                                                                                                                                                                          Sequence 2487 AA;
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ABU65149 standard; protein; 2498 AA.

RESULT 29 ABU65149 20-MAY-2003 (first entry)

ABU65149

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NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer; hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine; human.
                          WO200272757-A2
                   Homo sapiens.
                                       08-MAR-2002;
                                 19-SEP-2002
                                                                                                                                                                                                                         18-OCT-2001;
                                                                                                         23-MAR-2003
                                                                                                                      28-MAR-2001
                                                                                                                                 30-MAR-200
                                                                                                                                                                                          JUN-2001
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                                                                                                     2-MAR-2
                                                                                                                                       02-APR-2
                                                                                                                                                        02-MAY-2
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Human; NOVX; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; cancer, neurodegenerative disorder; Alzheimer's disease; immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease.
                                                                                                                                                         ADN61949 standard; protein; 2498 AA
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2001US-0275235P.
2001US-0275578P.
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2001US-0299027P
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08-MAR-2001;
08-MAR-2001;
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13-MAR-2001;
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14-MAR-2001;
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                                             557 1
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                                                                                                                              RESULT 30
                                                                                                                                            ADN61949
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                                                                                                                                                                                                                                                                                                                                                                                             cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypotrension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABU65041-ABU65218 represent the NOVX polypeptides encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 LKANAEYIKMADHYVPVPGGPNNNNYANVELIVDIAKRIPVQAVWAGWGHASENPKLPEL 353
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                                                                                                                                                         , Anderson D;
Alsobrook JP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOVX polypeptides and polynucleotides, useful for preventing or treatia disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma.
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                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel human NOVX polypeptides which have
                                                                                , Shenoy SG, Taupier RJ, Pena Cba, Ji W, Gorman L, Miller CE, Kekuda R; .i E, Vernet CAM, Guo X, Tchernev V; .i E, Vankar UM, Gerlach V, Liu Y, A
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                                                                                                            Lorunsen BD, Gusev V, Ji W, Gorman L, Miller Patturajan M, Gangolli E, Vernet CAM, Guo K, Fernandes ER, Casman SJ, Malyankar UM, Gerlach Spaderna SK, Catterton E, Burgess C, Leite M, Lepley DM, Rieger DK;
                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 313-314; 1103pp; English.
 03-DEC-2001; 2001US-0338092P.
04-DEC-2001; 2001US-033718SP.
03-JAN-2002; 2002US-0345705P.
07-MAR-2002; 2002US-0092900.
                                                                              (CURA-) CURAGEN CORP
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16-AUG-2001; 2010US-0312919; 16-AUG-2001; 2010US-0318462P. 10-SEP-2001; 2001US-0318462P. 27-SEP-2001; 2001US-0325681P. 27-SEP-2001; 2001US-0325681P. 18-OCT-2001; 2001US-0335301P. 14-NOV-2001; 2001US-0333272P. 14-NOV-2001; 2001US-0333272P. 14-NOV-2001; 2001US-0333272P. 14-NOV-2001; 2001US-0333272P. 14-NOV-2001; 2001US-0333272P. 14-NOV-2001; 2001US-0333272P. 14-NOV-2001; 2001US-0333272P. 14-NOV-2001; 2001US-0333272P. 14-NOV-2001; 2001US-0333272P. 14-NOV-2001; 2001US-0333272P. 14-NOV-2001; 2001US-0333272P. 21-NOV-2001; 2001US-0333272P. 21-NOV-2001; 2001US-0333272P. 21-NOV-2001; 2001US-03332094P.
                2001US-0309198P
                                                                                                                                  03-DEC-2001; 2001US-0337426P
03-DEC-2001; 2001US-0338092P
04-DEC-2001; 2001US-033718P
03-JAN-2002; 2002US-034718P
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CASMAN S J.
MALYANKAR U M.
GERLACH V.
                                                                                                                                                                                                                                                                               PATTŮRAJAN M.
GANGÖLLI E A.
VERNET C A M.
                                                                                                                                                                                                                                                                                                                                                                                                           LSOBROOK J P.
                                                                                                                                                                          PADIGARU M.
SPYTEK K A.
SHENOY S G.
TAUPIER R J.
PENA C E A.
LI L;
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GUSEV V Y.
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MILLER C E.
KEKUDA R.
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TCHERNEV V T.
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SPADERNA S K.
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ZHONG H.
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RIEGER D K.
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pytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li I Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R; Gangolli EA, Verner CAM, Guo KS, Tchernev VT; Casman SJ, Malyankar UM, Gerlach V, Liu Y; Spaderna SK, Catterton E, Leite MW, Zhong H; Lepley DM, Rieger DK, Burgess CE; Spaderna SK, Lepley DM, Spytek KA, Gusev VY, Patturajan M, C Fernandes ER, C Anderson DW, S Alsobrook JP, Padigaru M, Zerhusen BD,

WPI; 2004-225693/21. N-PSDB; ADN61948.

New NOVX polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; SEQ ID NO 218; 786pp; English.

The invention relates to an isolated polypeptide (designated NOVX, or NOV1-NOV127) comprising a sequence selected from 178 fully defined amino acid sequences (and their mature forms, variants and fragments). Also

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included are an isolated nucleic acid molecule encoding NOVX, a vector comprising the nucleic acid, a cell comprising the vector, methods for determining the presence or amount of the polypeptide or the nucleic acid molecule in a sample, methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first manmalian cubject, a method for identifying an agent that binds to the above polypeptide or nucleic acid molecule in a first manmalian subject, a method for identifying a potential therapeutic agent for cupe in the treatment of a pathology that is related to abbrrant care applyable or a modulator of activity or of latency or predisposition to screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide and a method for modulating the activity of the polypeptide cited above. The composition and methods are useful for diagnosing, preventing or treating diseases such as a pathology, associated diseases, observative diseases, anorez-associated cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or Parkinson's disease, immune disorders, heamacopoietic disorders, chromosome mapping, tissue typing, preventive medicine and chromosome mapping, tissue typing, preventive medicine and chromosome mapping, the polypeptides are also useful as vaccines. The present sequence represents a NOVX protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QG-F 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEVPGSPVFVMKLAGOARHLEVQLLADOYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 AIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437 ITAENPDIGFKPGMGALTELNFRSSISTWGYFSVGISGALHEYADSQFGHIFAYGADRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.4%; Score 1756.5; DB 8; Length 2498; 63.0%; Pred. No. 1.2e-154; ive 75; Mismatches 109; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKT-QRKPQPQGHVVACR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ47656 standard; protein; 774 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 63.0
Matches 342; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
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ADJ47656
ID ADJ47
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318 DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 AISNMVVALKELSIRGDFRTTVEYLINLLETESFONNDIDTGWLDYLIAEKV-QEKPDIM 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                     482 SEIPGSPIFLMKIAQHARHLEVQILADQYGNAVSLFGRDCSIQRRHQKIVEEAPATIAPL
                                                                                                                                                                                                                                                                                                                                                                                                              653. ITSENPDEGFKPSSGTVQELNFRSSKNVWGYFSVAATGGLHEFADSQFGHCFSWGENRKE
                       LTVSDDVYQQACIHTABEGLEXAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL
                                                                                                                                                                                                                             542 AIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL
                                                                                                                                                                                                                                                                                           378 PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKT-QRKPQPQGHVVACR
                                                                                                                                                                                                                                                                                                                     437 ITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PRO nucleic acid or polypeptide, useful for preparing a
pharmaceutical composition for diagnosing or treating psoriasis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schoenfeld J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; SEQ ID NO 28; 3069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN03634 standard; protein; 2206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antipsoriatic protein sequence #14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jackman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2003; 2003WO-US030907.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-305105/28.
N-PSDB; ADN03633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2206 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel peptide (I) comprising an acetyl CoA carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxylase (arboxylase domain, and having a functional blocin carboxylase domain. A peptide of the invention is useful for identifying Acetyl CoA carboxylase inhibitors or activators, which involves combining the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding indicating the compound is or assay to detect inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity. A peptide of the invention is also useful for carboxylase activity, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase compound binds to the biotin carboxylase compound binds to the biotin carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carboxylase domain, the presence of binding indicating the compound is or may be fungicide, employing the identified compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound that inhibits Acetyl CoA carboxylase activity. The present sequence represents the human ACC2 BC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QG-F 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biotin binding domain and carboxy transferase domain, and having functional biotin carboxylase domain, useful for identifying ACCase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 774;
                                                                                                                                   ACCase, Acetyl CoA carboxylase, carboxy transferase domain,
biotin carboxylase domain; BC domain; fungicide, human, ACC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.8%; Score 1738; DB 8; Length 77 62.8%; Pred. No. 9.1e-154; ive 76; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weatherly SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; SEQ ID NO 12; 56pp; English
                                                                                        Human ACC2 BC domain SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                         04-AUG-2003; 2003WO-US024356
                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-2002; 2002US-0401170P
                                          (first entry)
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Best Local Similarity 62.8'
Matches 341; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   (CROP-) CROPSOLUTION INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Volrath SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitors/activators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-180421/17.
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                                                                                                                                                                                                                                                WO2004013159-A2.
                                                                                                                                                                                                     Homo sapiens
                                             06-MAY-2004
                                                                                                                                                                                                                                                                                              12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elich TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
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ADJ47656
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                                                                             VDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQ 173
                                                                                         HADVPCMPWSGTGIKETWMSD---QGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIK 230
                                                                                                                                  ASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAI 290
                                                                                                                                                                                   238
                                                                                                                                                                                                   SIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPES 350
                                                                                                                                                                                                                         297
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                                                                                                                                                                                                                                                                                     470
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                                                           9
                                                  GBFAFLELNPRLOVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVI
                                                                                                                                                                                                                                                        54 IRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLI
                                                                                                                                                                                                                                                                                   DFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSV
                                                                                                                                                                                                                                                                                                                           GTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAF
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acetyl-coenzyme A carboxylase, acetyl-CoA carboxylase,
metabolic syndrome; diabetes, obesity; cardiovascular disease,
atherosclerosis; depression; cancer; hyperlipidaemia; dyslipidaemia;
hypertension; hyperuricaemia; renal disfunction;
                     13;
   2206;
   Length
                     98; Indels
  DB 8;
58.4%; Score 1697.5; DB 8 63.7%; Pred. No. 3.4e-149; ive 74; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; carboxyltransferase domain; CT domain;
                                                                                                                                                                                                                                                                                                                                                                                       499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human acetyl-coenzyme A carboxylase - ACC2
                                                                                                                                                                                                                                                                                                                                                                  ESNKITTGWLDGLIQDRLTAERPPADLAV 559
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2003US-0459464P.

2003US-0491640P.

2003US-0514636P.
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         Best Local Similarity 55... Matches 324; Conservative
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27-OCT-2003;
09-JAN-2004;
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31-MAR-2003;
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 Query Match
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                                                                                                                                                             The invention comprises a crystallisable composition containing a carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-COA) carboxylase. The composition of the invention is useful for treating: metabolic syndrome, diabetes, obesity, cardiovascular disease, atherosclerosis, depression, cancer, hyperlipidaemia, dyslipidaemia, hypertension, hyperuricaemia and renal disfunction. The present amino acid sequence represents a human acetyl-COA carboxylase of the invention.
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                                                                                               obesity,
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                                                                             New crystallizable composition comprising a carboxyltransferase dacetyl-coenzyme A (CoA) carboxylase, for treating e.g. diabetes, cardiovascular disease, atherosclerosis, or cancer.
                                                                                                                                                                                                                                                                                                       57.4%; Score 1669.5; DB 8; Length 2483; 60.8%; Pred. No. 1.8e-146; 1ve 79; Mismatches 117; Indels 17;
                                                                                                                                      Example 4; SEQ ID NO 9; 195pp; English
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The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual saltered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic sold molecule comprising at least a contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequence given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antigon-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about is antigon-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about is and 1000 nucleotides in Ength, a kit for detecting an SNP in a nucleic acid molecule, a method of detecting an SNP in a nucleic acid molecule, a method of detecting an surfaction. The novel detecting a variant polypeptide; and an encydence method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method is seful in identifying an individual who has a increased or
                                         Human myocardial infarction-associated gene derived protein, SEQ ID 1170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associated gene containing one or more SNP's of the invention. Note: Thi sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                       detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; SEQ ID NO 1170; 145pp; English
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                                                                                                            cardiant; gene therapy; human
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10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                                                                                                                                                                  22-DEC-2003; 2003WO-US040978
(first entry)
                                                                                     Myocardial infarction;
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SQ Sequence 2483 AA;

Query Match

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Best Local Similarity 60.8%; Pred. No. 1.8e-146;

Matches 330; Conservative 79; Mismatches 117; Indels 17; Gaps 8;

Qy 22 ASPVADFIRKQGHSVITKVI.ICNNGIAAVKEIRSIRKWAYETFGDERAIEFTWATPED 81
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82 LKVNADYIRMADQYVEVPGGSMNNYANVDLIVDVAERAGVHAVMAGWGHASENPRLPES 141

244 ASP-AEFVTRFGGDRVIEKVLIANNGIAAVKCMRSIRRWAYEMFRNERAIRFVRMVTPED

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196 420 316 Identifying a modulator of whole body insulin sensitivity of an animal by determining the AMP-dependent protein kinase or acetyl CoA carboxylase activity or free fatty acid level or oxidation in the animal administered EDARESMEKAAVRLAKLYGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVN 376 599 436 652 496 303 LKANAEYIKMADHYGPAPGGPNNNNYANVELIVDIAKRIPLQAVWAGWGHALENPKLPEL 362 The invention comprises a method of identifying a compound that enhances or reduces whole body insulin sensitivity of an animal. The method ARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIODRLTAERPPAD FLTVSDDVYQQACIHTABEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAV LGEVPGSPVFVWKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAP 481 QSEIPGSPIFLMKLAQHARHLEVQILADQYGNAVSLFGRDCSIQRRHQKIVEEAPATIAP LAIFEFMEQCAIRLAKTVGYVSAGTVBYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVN 377 IPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACR ITAENPOTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSOFGHIFAYGADRSE LAASKHKIIFIGPPG-SAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD-obesity; diabetes; atherosclerosis; heart disease; ACC2. Cooney GJ, Molero-Navajas JC; Disclosure; SEQ ID NO 4; 296pp; English. AEA33628 standard; protein; 2483 AA. GARV-) GARVAN INST MEDICAL RES Human ACC2 protein - SEQ ID 4. 14-NOV-2003; 2003AU-00906285. 14-NOV-2003; 2003AU-00906286. 15-NOV-2004; 2004WO-AU001572. (first entry) WPI; 2005-386363/39. LAV 559 LGV 774 WO2005047525-A1. with a compound. Homo sapiens 28-JUL-2005 36-MAY-2005. James D, 363 197 257 317 437 497 713 142 772 AEA33628 a CCXSXLTLLLXBXBXBXBXBXBXBXSXXXXXBXCCCX Š 셤 8 q ò g ठे 요 ò 셤 8 셤 ò g à

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involves administering a compound to a non-human animal, isolated tissue or cell having reduced expression of functional multi-adaptor protein Cbl, and determining the activity of acetyl CoA carboxylase (ACC) and/or amount of phosphorylated ACC enzyme in the animal, tissue or cell. The method is useful for identifying a compound that enhances or reduces whole body insulin sensitivity of an animal, and for preparing a composition for the treatment of obesity, diabetes, atherosclerosis and heart disease. The present amino acid sequence represents a human ACC2
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                                                                                                                                                                57.4%; Score 1669.5; DB 9; 60.8%; Pred. No. 1.8e-146; ive 79; Mismatches 117;
                                                                                                                                                                              Best Local Similarity 60.8
Matches 330; Conservative
                                                                                                                                       Sequence 2483 AA;
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biotin carboxylase domain; BC domain; fungicide.
                                                                                                                                                                                                   P. infestans ACCase BC domain SEQ ID NO:4
                                                                                                                                   ADJ47652 standard; protein; 555 AA
                                                                                                                                                                                                                                                         Phytophthora infestans
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ADJ47652

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254

317 PTQEVWEKNARAATRLAQEVEYVNAGTVEYLFSELPEDNGNSFFLELNPRLQVEHPVTE 376

APEDARESMEKAAVRLAKLVGYVSAGTVEWLYS--PE--SGEFAFLELNPRLOVEHPTTE

315

WO2004013159-A2

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The invention relates to a novel peptide (I) comprising an acetyl CoA carboxylase (AcCase) having a deleted biotin binding domain, having a clasted carboxylase domain, and having a functional biotin carboxylase domain. A peptide of the invention is useful for identifying Acetyl CoA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding compound in carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity. A peptide of the invention is also useful for carboxylase activity to binding to biotin carboxylase compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or arboxylase domain, the presence of binding indicating the compound is or arboxylase domain, the presence of binding indicating the compound is or arboxylase domain, the presence of binding indicating the compound is or arboxylase domain, the presence of binding indicating the compound is or arboxylase domain, the presence of binding indicating the compound is or arboxylase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 may be fungicide, employing the identified compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound that inhibits Acetyl CoA carboxylase activity. The present sequence represents an ACCase BC domain of the invention.
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                                                                                                                                                                                                                                                                                                                                                        Novel peptide comprising acetyl CoA carboxylase (ACCase) having dele
Siotin binding domain and carboxy transferase domain, and having
functional biotin carboxylase domain, useful for identifying ACCase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
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                                                                                                                                                                                                                                                   Weatherly SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; SEQ ID NO 4; 56pp; English
                                                                                                                                                                                                                                                                                                                                                           Novel peptide comprising acetyl Co
biotin binding domain and carboxy
                                                                                04-AUG-2003, 2003WO-US024356
                                                                                                                                                                                          (CROP-) CROPSOLUTION INC
                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibitors/activators
                                                                                                                                                                                                                                                                                                    WPI; 2004-180421/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of nucleotide sequences given in the specification in the individual's nucleotide sequence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention altered risk for myocardial infarction in the individual. The invention the specification or its complement and encoding any one of the amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding comprising an amino acid sequence given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polymucleotide, a buffer and an enzyme; a method of detecting an SNP in a mucleic acid molecule; a method of detecting or preventing comprising in method for identifying an agent useful in treating or preventing an amount in the moule of method for identifying an agent useful in treating or preventing an contraction. The novel detection method has cardiant activity.
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                                                                                                                                                                                                                                                                                                                   Human myocardial infarction-associated gene derived protein, SEQ ID 1167
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nucleotide polymorphism in
                               ||:| |||||:| || ||:| ||:| ||:| ||:|::
HVIAARITAEDPNAGFQPISGAIQELNFRSTPDVWGYFSVDSSGQVHEFADSQIGHLFSW
                                                                                                                                                                                                                                                                                                                                                 detection; single nucleotide polymorphism; SNP;
             MVSGVNI PAAQLQVAMGI PLYSIRDIRTLYGMDPRGNEVI DFDFSSPESFKTQRKPQPQG
                                                                    HVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acids of the invention may be used in gene therapy. The
                                                                                                                            541
                                                                                                                                                         539
                                                                                                                                            SPTREKARRANVLALKELSIRGDIHTTVEYIVNMMESDDFKYNRISTSWLD
                                                                                                                            GADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying an individual who has an altered myocardial infarction by detecting a single n the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; SEQ ID NO 1167; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iakoubova 0;
                                                                                                                                                                                                                              ADQ39504 standard; protein; 1096 AA
                                                                                                                                                                                                                                                                                                                                                                 cardiant; gene therapy; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
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                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                 Myocardial infarction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (APPL-) APPLERA CORP
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10-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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ADQ39504
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                                                                                                                                                                                                                                                                                                                                         303
                                                                                                                                                                                                                                                                                                                                                                              LKYNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                                                                                                                                                                                                                                                                                                                                       DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QG-F 197
method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction associated gene containing one or more SNF's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO, website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL
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                                                                                                                                                                                                                                                                                                                     542 AIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADDVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498 RKOMVISLKELSIRGDFRITVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTÖRKPQPQGHVVACRI
                                                                                                                                                                                                                                                                                                 ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 TAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                           Length 1096;
                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                   93;
                                                                                                                                                                                                           54.7%; Score 1591.5; DB 58.1%; Pred. No. 1e-139; ive 65; Mismatches 93
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les 315; Conservative
                                                                                                                                                                        Sequence 1096 AA;
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                                                                                                                                                                                                             Query Match
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Matches
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Pred. No. 4.1e-139;
                                                                                                                                                                                            54.7%; Score 1591.5; 58.1%; Pred. No. 4.1e
                                                                                                                                                                                                       65; Mismatches
                                                                              Claim 20; Page 678; 765pp; English
         16-APR-2001; 2001WO-US008656
                   18-APR-2000; 2000US-00552929 26-JAN-2001; 2001US-00770160
                                           Tang YT, Liu C, Drmanac RT
                                                                                                                                                                                                                                                                                                                                                   PAAQLQ-----
                                                                                                                                                                                                       Conservative
                                                     WPI; 2001-611725/70.
                                                                                                                                                                                                 Best Local Similarity
Matches 315; Conser
                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                  Sequence 2486 AA;
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                                                                                                                                                                                                                                                          The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide to aberrant expression or physiological interactions of the polypeptide with a proteins the proteins are useful for producing the proteins. The proteins the proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and simulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid sequences of novel human expression and the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      571 AIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTVSDDVYQQACIHTAEBGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DARBSMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---OG-F 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                         Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 TAENPDIGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 2486;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 SLVAMATPEDMRINAEHIRIADQFMQVPGGTNNNNYANVHLIVEMAEATGVDAVWPGWGH 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETM 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                        498 RKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acetyl CoA; carboxylase; lipid; fatty acid; biosynthesis; metabolism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acetyl CoA-carboxylase from plants, e.g. brassica napus - is useful modifying the oil and fatty acid prodn. in plants or for conferring resistance to certain herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.5%; Score 1583; DB 2; Length 2 llarity 53.5%; Pred. No. 2.2e-138; Conservative 105; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                            AAR67819 standard; protein; 2240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 7; 31pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93DE-04317260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93DE-04301694
                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Acetyl CoA carboxylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-236136/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2240 AA;
                                                                                            558 AV 559
                                                                                                                                         749 GV 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica napus.
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                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
01-MAR-1995
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                                                                                                                                                                                                                                                                                                           AAR67819;
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VTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEM 371
                                                                 VSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGH 431
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                                                                                                                                 VVACRITAENPDIGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYG 491
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PPGSSLVTIPEEMYRQACVYTTEEAVASCQVVGYPAMIKASWGGGGKGIRKVHDDDEVRA 339
                                                                                                                                             LYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIBEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequenc from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; SEQ ID NO 462; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                       Herbicidally active polypeptide SEQ ID NO 462
                                                                                                                                                                                                                                                                                                                                                          Herbicidal; plant; agriculture; herbicide
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                                                                                                                                                                                                                                                                               ABB91251 standard; protein; 2359
                                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fietjen K, Weidler M;
                                                                                                                                                                                                             559
                                                                                                                                                                                                                               RPPWYLSV 647
                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-269010/31.
                                                                                                                                                                                                             RPPADLAV
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                                                                                                                                                                                                                                                                                                                                                                                               WO200210210-A2
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The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using-suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as

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Sequence 2359

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                                                                                       RAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAG 128
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                                            IGGNPLETAPASPVA---DFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDE
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                      Сарв
                      35;
 Length 2359;
54.4%; Score 1581.5; DB 5; Length
53.3%; Pred. No. 3.3e-138;
ive 95; Mismatches 137; Indels
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Query Match
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Matches 305; Conservative
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